

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 13:52:37 ; Search time 96 Seconds
(without alignments)
1560.378 Million cell updates/sec

Title: US-09-923-444A-2
Perfect score: 3817
Sequence: 1 MPKSKVTQREHSHVYTES.....NPNGPYGRGYLLASTPESEL 727

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.rodent.*
- 12: sp.virus.*
- 13: sp.vertebrate.*
- 14: sp.unclassified.*
- 15: sp.rvirus.*
- 16: sp.bacteriap.*
- 17: sp.bacteriap.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1495.5	39.2	744	5 Q9V818	Q9V818 drosophila
2	1337.5	35.0	634	11 Q9D687	Q9D687 mus musculus
3	1326	34.7	615	11 Q88576	Q88576 mus musculus
4	1323	34.7	616	4 Q8TF10	Q8TF10 homo sapien
5	1307.5	34.3	592	4 Q9NP91	Q9NP91 homo sapien
6	1305	34.2	662	5 Q9W4S0	Q9W4S0 drosophila
7	1303.5	34.1	592	11 Q8VDB9	Q8VDB9 mus musculus
8	1302.5	34.1	616	11 Q64093	Q64093 rattus norv
9	1302.5	34.1	635	11 Q91WT6	Q91WT6 mus musculus
10	1300.5	34.1	635	11 Q88575	Q88575 mus musculus
11	1294.5	33.9	615	11 Q62687	Q62687 rattus norv
12	1282	33.6	628	4 Q96N87	Q96N87 homo sapien
13	1141	29.9	577	11 Q91XG6	Q91XG6 mus musculus
14	1032	27.0	791	11 Q91ZQ2	Q91ZQ2 mus musculus
15	1024	26.8	397	4 Q9BYZ7	Q9BYZ7 homo sapien
16	1008.5	26.4	631	5 Q9NB97	Q9NB97 drosophila

17	1008.5	26.4	631	5 Q961H9	Q961H9 drosophila
18	1007	26.4	629	13 Q90ZV1	Q90ZV1 brachydenio
19	1001	26.2	576	5 Q9V7R0	Q9V7R0 drosophila
20	1000.5	26.2	642	4 Q9UN76	Q9UN76 homo sapien
21	996.5	26.1	633	11 Q8VC47	Q8VC47 mus musculus
22	987.5	25.9	638	11 Q9D317	Q9D317 mus musculus
23	987.5	25.9	638	11 Q9JMA9	Q9JMA9 mus musculus
24	987.5	25.9	638	11 Q91V60	Q91V60 mus musculus
25	986.5	25.8	617	6 Q9MXW8	Q9MXW8 macaca mula
26	985.5	25.8	628	4 Q96KH8	Q96KH8 homo sapien
27	983	25.8	630	13 Q42482	Q42482 rana catesb
28	976.5	25.6	619	11 Q9JJ41	Q9JJ41 mus musculus
29	976.5	25.6	619	11 Q9R0X6	Q9R0X6 mus musculus
30	975.5	25.6	617	11 Q8R212	Q8R212 mus musculus
31	974.5	25.5	602	4 Q8TCC2	Q8TCC2 homo sapien
32	969.5	25.4	635	13 Q9DGN5	Q9DGN5 gallus gall
33	965.5	25.3	1201	5 Q9W1J0	Q9W1J0 drosophila
34	965	25.3	617	11 Q63380	Q63380 rattus norv
35	964.5	25.3	638	11 Q9R183	Q9R183 mus musculus
36	961	25.2	289	4 Q9H9F5	Q9H9F5 homo sapien
37	961	25.2	289	4 Q8TBM6	Q8TBM6 homo sapien
38	961	25.2	640	11 Q8VBW1	Q8VBW1 mus musculus
39	958	25.1	620	6 Q9GJT6	Q9GJT6 macaca fasc
40	955.5	25.0	515	13 Q918Q2	Q918Q2 coturnix co
41	954	25.0	620	6 Q9GJT5	Q9GJT5 saimiri sci
42	953	25.0	611	13 Q91502	Q91502 torpedo mar
43	952.5	25.0	567	11 Q9WTR3	Q9WTR3 rattus norv
44	952.5	25.0	597	11 Q9WTR4	Q9WTR4 rattus norv
45	952.5	25.0	614	11 Q8VCS9	Q8VCS9 mus musculus

ALIGNMENTS

RESULT 1

ID	Q9V818	PRELIMINARY;	PRT;	744 AA.
AC	Q9V818;			
DT	01-MAY-2000 (TReMBLrel. 13, Created)			
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)			
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)			
DE	C65226 protein.			
GN	C65226.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY;			
RX	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,			
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Glodis A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,			
RA	Jatelli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			

QY 516 GNYFVTMEDDYSATPLPLIVILENAVIAWYGPCKFMQELTEMLGFRPYRYFYFMWKFV 575
 Db 463 GGYWLEIFDSFAASNLIIIFAFMEVGVVHIIYGMKRFCDIEEMTGRRLGQWQYTRVV 522
 QY 576 SPLCMVLTASIIOLGTVPAYSAW-----IKERAAERYLYFPNPMALLITLIVV 627
 Db 523 SPMLLGIFLSYVILLIQTSPSYKAWNPQYEHFPSREK-----FYPGWVQVTCVLLSPL 577
 QY 628 ATLPIPVVFLRHFLHSDGNTLSVSK---KARMDKDISLEEN 670
 Db 578 PSLWVPGVALAQ---LLS-----QYQKRWKATHLESGLKQES 612

RESULT 4
 Q8TF10 PRELIMINARY; PRT; 616 AA.
 AC Q8TF10; Q8TF10; Q8TF10; Q8TF10; Q8TF10; Q8TF10; Q8TF10; Q8TF10; Q8TF10; Q8TF10;
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Neurotransmitter transporter RB21A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou Y., Yu L., Zhao S.Y.;
 RT "Cloning of a new human cDNA similar to Rattus norvegicus
 neurotransmitter transporter RB21A."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ding J.B., Yu L., Zhao S.Y.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF125107; AAL7594.1;
 SQ SEQUENCE 616 AA; 68365 MW; D3DF0C282A1D0237 CRC64;

Query Match 34.7%; Score 1323; DB 4; Length 616;
 Best Local Similarity 41.7%; Pred. No. 1.2e-98;
 Matches 263; Conservative 125; Mismatches 199; Indels 44; Gaps 11;

QY 25 LALEPVDYKQSVLVNAGBAGKQKAVEEELDAEDPAWNSKIQYIIAQIGFSGVGLGNW 84
 Db 3 LAIKPASCDDPRAGAEAGAMEKA-----RPLWANSIQFVACISYAVGLGNVW 53
 QY 85 RPYLCOKNGGAYLPVYLIIITIGIPLFLELAVQQRIRGSGVWHYICPRLOGIGF 144
 Db 54 RPYLCQMGGSGLFVYIIMLIVEGMLLYLELAVQGRMQSGISGAWRTISPLSGGV 113
 QY 145 SSCIVCLFVGLYNYVLIIGWSIFVFKSFQYPLPWSBCPVVRGNSVAVVAECEKSSATY 204
 Db 114 ASVVVFFLSMYNYVINAFAWFLHSDFOPLPWSVCLP--NGNHTGYDECEKASSTQY 171
 QY 205 FWRALDISDSISSGGLNWKMTCLLVVWSIGGMVAGKIQSSGKVMYFSSLPFYVVL 264
 Db 172 FWRKTLNISPLSQENGQVQWEPALCLLAWLVVYLILRGTESTGKVVYFTASLPYCVL 231
 QY 265 ACFLVRGLLRGAVDGIILHMTFKLVKMLDQVWREAVATQVFGGLGFGGVIVFSSYNK 324
 Db 232 IYILRGTLHGATNGLMFMFTPKLEQLANPRAWNAATQIFSLGLFGFSLTAFASYNE 291
 QY 325 QDNCHFDGALVSINFTSVLATLVFVVLGFKANIMNEKCVENAELKILVNTNVL 384
 Db 292 PSNNCKHAIIVLSINLSIFASIVTSIYGFKATFVYENCL-----KVSLLLTNTFD 346
 QY 385 RDLPPHVNFLTKDYEMDNVNTWKEDQFSAL--GLDPCLLLEDKSVQGTGLAF 442
 Db 347 -----LEDGFLASNLLEQVKGVLASAYPSKYSEMFQIKNCSLESLDTAVQGTGLAF 399
 QY 443 IAFTEAMTHFTSPFWSVFFMLINLGLSGMIGMTPIID----TSKVPKEMFTV 498

Db 400 IVYTEALKNMEVSOLWSVLYFFMLMLGICSMGLNCTAAILPLTDSKISSLHPKEATSG 459
 QY 499 GCCVFTFLVGLLFVORSGNVFVTMDDYSATPLPLIVILENAVIAWYGPCKFMQELTE 558
 Db 460 LVCLVNCAIGMVFTEAGNWFDFNDYVATLSLLLVLTIVETIACVYVGLRRFESDLKA 519
 QY 559 MLCGRPYRYFYMKKFSPLCMA---VLTTASIIOLGTVPAYSAWIKERAAERYLY--- 612
 Db 520 MTGRASVWKMVAGVSPLLVSLFVLYSDYILTGL--KYQAW---DASQGLVTKD 574
 QY 613 FPNPMALLITLIVATPLIPV-----VFVLR 639
 Db 575 YPAVALAVIGLLVASSTMCIPLAALGTFVQR 605

RESULT 5

Q9NP91 PRELIMINARY; PRT; 592 AA.
 AC Q9NP91; Q9NP91; Q9NP91; Q9NP91; Q9NP91; Q9NP91; Q9NP91; Q9NP91; Q9NP91; Q9NP91;
 DT 01-OCT-2000 (T-EMBLrel. 15, Created)
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Sodium- and chloride-dependent transporter XTRP3.
 GN XTRP3 OR XTR3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RA Kiss H.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-315 FROM N.A., AND TISSUE SPECIFICITY. 1
 RX MEDLINE=99131080; Pubmed=9932288;
 RA Nash S.R., Giros B., Kingsmore S.F., Kim K.M., El-Mestikawy S.,
 Dong Q., Fumagalli F., Seldin M.F., Caron M.G.;
 RT "Cloning, gene structure, and genomic localization of an orphan
 transporter from mouse kidney with six alternatively-spliced
 isoforms."
 RL Recept. Channels 6:113-128(1998).
 RN [3]
 RP SEQUENCE OF 232-592 FROM N.A.
 RA Pluvinet R., Estivill X., Escarceller M., Sumoy L.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; XTR3 (SHOWN HERE) AND XTR3A; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: KIDNEY AND SMALL INTESTINE.
 CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
 CC FAMILY (SNF).
 DR EMBL; AJ276207; CAB99310.1;
 DR EMBL; AJ276208; CAB99311.1;
 DR EMBL; AJ289880; CAB96872.1;
 DR EMBL; AL389979; CAB97535.1;
 DR EMBL; AF075260; AAC27755.1;
 DR InterPro: IPR000175; Na/ntran_symport.
 DR Pfam: PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR ProDom: PD000448; Na/ntran_symport; 2.
 DR PROSITE; PS00610; NA_NEUROTRAN_SYMPT_1; FALSE_NEG.
 DR PROSITE; PS00754; NA_NEUROTRAN_SYMPT_2; FALSE_NEG.
 DR PROSITE; PS0267; NA_NEUROTRAN_SYMPT_3; 1.
 KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
 KW Symport; Alternative splicing.
 FT DOMAIN 1 42
 FT TRANSMEM 43 63
 FT DOMAIN 64 79
 FT TRANSMEM 80 100
 FT DOMAIN 101 107
 FT TRANSMEM 108 128
 FT DOMAIN 129 165
 FT TRANSMEM 166 186
 FT TRANSMEM 187 196
 FT TRANSMEM 197 200


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Qy 154 GLYNNVILGWSIFPFKFOYPLPNSCPV-VANGSVAVVAEACEKSSATTFFWYREALD 212
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 148 ALYNTTIIIAWCLIIYLHSPFSLPWADCTRLYKNTFYDHEPECVASSPTQFYWYRTTLQ 207
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 213 LSDSTSSEGLNKKWTKLCLLVVMSIGGMVAGVGIOSSGKVMYFSSLPVAVLACFLVRGL 272
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 208 CSESDMPEFNFNHMAIALIVSWFLVYICMVGITSSGKIVMTAIFPVVLIIFFERGI 267
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 273 LLRGAVDGLIHMTFKLVMKLDPPQVWREVATOVFFGLGLGFGGVIVFSSYNKODNCHFD 332
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 268 TLKGAADGVHLETPRWETLPVWVLEAGTOIFFSLGLAFGLIAFSSYNPANNCYRD 327
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 333 GALVSFINFTSVLATLVVFLVGLPKANIMKCVVENAEKILGYLNTNVLSDRLIPPHV 392
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 328 ALLVSLNCTGSMFAGVGVVIGFATATDFRCTEERNLVA-----Q 371
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 393 NPSHLTTTKDYMDMNDVIMTKEDQFSAALGDLPCLEDELKSVQGTGLAFIATEAMTHF 452
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 372 NKTH-----NLPVCDLQTELANSASGTGLAFIIFTEAINQF 407
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 453 PTSPFWSVFFMLNLGLGSMIGTWAGITPTIDTS---KVPKEMFTVCCCVFTFLVGL 509
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 408 PQAQLWAVLFFLMLFTLGDGDSQFTLEGVVTSLVDMKLPNLPKXYIVGALCFSCCTISM 467
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 510 LFVQSGNFTVMTFDYSATPLTLVILENIAVAMIYGPKEQELTEMLGPRPYRYF 569
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 468 CFANGAGSVIFQLMDSFAGNFPLLIITALECLISYIYGVRRFSDDIEMTSGRPNFYW 527
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 570 YMKKVFSPICMAVLTASTIQLGVTTPAYSANIKKEAERYLYFPNPMALLITLIVAT 629
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 528 FCWKYLLSPCAMVTILLASFYQLLTGESSYPAWIGSKGATEGMEWPHCIIVVAFLLILSI 587
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 630 LPIPVVFLR 639
    ||||| || | | | | |
Db 588 LWIPIVAVLR 597
    ||||| || | | | | |

RESULT 7
Q8VDB9 PRELIMINARY; PRT; 592 AA.
AC Q8VDB9;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE x transporter protein 3 similar 1.
GN XTRP31.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Kiss H., Darai E., Kiss C., Kost-Alimova M., Klein G., Dumanski J.P.,
RA Imreh S.;
RT "Comparative Sequence Analysis of the Common Eliminated Region 1
RT (C3ER1) on Human Chromosome 3p21.3 with the Orthologous Regions on
RT Mouse Chromosome 9F.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ428067; CAD20989.1; -.
DR InterPro; IPR000175; Na/ntran_symport.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSMPORT.
DR ProDom; PD000448; Na/ntran_symport; 2.
DR PROSITE; PS0267; NA_NEUROTRAN_SYMP_3; 1.
DR PROSITE; PS0267; NA_NEUROTRAN_SYMP_3; 1.
SQ SEQUENCE 592 AA; 66178 MW; 547B9F8C0B7A99AA CRC64;

Query Match 34.1%; Score 1303.5; DB 11; Length 592;
Best Local Similarity 44.0%; Pred. No. 4.2e-97;
Matches 259; Conservative 115; Mismatches 183; Indels 31; Gaps 11;

Qy 60 RPAWNSKLQVILAGIGFSVGLGNIRWRFYLCQKGGGAYLVPLVLLIIIGIPLFFLELA 119

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Db 5 RPQGHPLQFVACISYAVGLGNVWRFPYLCOMYGGGSLVPYIIMLVIEGMPLLYLELA 64
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 120 VQQRIRGSGICWHYICPRIGGIFSSICVLCFLGLYNNVILGWSIFPFKFOYPLPWS 179
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 65 VQGRMROGSIAGAWRTIIPYLSGVGVASVVSFFLSMYNNVINAMGWFYLFHGFQDPLWS 124
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 180 ECPVVRNGSVAVVAEACEKSSATTFFWYREALDIDSISSEGLNKKWTKLCLLVVMSIGG 239
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 125 VCPL--NSNHTCYDECEKASSTQFYWRKTLNLSPSIOENGSGVQWEPALCLTAWLMVY 182
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 240 MAVKGIGQSSGKVMYFSSLPVAVLACFLVRGLLRGAVDGLIHMTFKLVMKLDPPQVWR 299
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 183 LCILRGTESTGKVVYFTASMPYCVLIILVLRGLTLHGATNGLMYMTPKMEQLANPKAWI 242
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 300 EVATQVFGGLGGGVIVFSSYNKODNKNHFDGALVSPINFEFTSVLATLVVFLVGLGFA 359
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 243 NAATQIFSLGLGFGSLAFASYNPSNCKQHAIVLSINSTSIFASIVFSIYGFKA 302
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 360 NIMKECVVENAEKILGYLNTNVLSDRLIPPHVNFHSLTKDKYMDMNDVIMTKEDQFSA 419
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 303 TFNYENCL---NKVI-LLLTN--SFDL-----EDGFLTVSNLEEVKNYLASTYPNKYSE 350
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 420 L--GLDPCLEDELKSVQGTGLAFIATEAMTHFTSPFWSVFFMLNLGLGSMIGT 477
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 351 VPHIRNCSLESELDVATQGTGLAFIVTEAKNMEVSQLWSVLYFFMLMLIGISMLGN 410
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 478 MAGITTPID----TSKVPKEMFTVCCCVFTFLVGLLFFVQSGNFTVMTFDYSATPLT 533
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 411 TAAITPLTDSKVISSYLPKKEAISGLVCLINCAVGAVFTMEAGNYWFDIFNDYAATLSLL 470
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 534 LIVILENTAVAMIYGPKEQELTEMLGPRPYRYFYMKKFYSPLCMA---VLTTASIIQ 590
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 471 LIVIVETIACVYVGLKRFESDLRAMTGRTLTSWYKWKVMAFVSPLLIVGLFIFLYSDIYL 530
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 591 LGVTPPAYSAWIKKEAERYLYFPNWP---MALLITLIVATLPIPV 635
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 531 TGTL--QYQW---DATQQLVTKDYPHALAVIGLLVASSMTCIFLV 573
    ||||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
Q64093 PRELIMINARY; PRT; 616 AA.
AC Q64093;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Sodium- and chloride-dependent transporter XTRP3 (NEUROTRANSMITTER
DE transporter RB21A).
GN XTRP3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA MEDLINE=95094940; PubMed=8001687;
RA Smith K.E., Fried S.G., Durkin M.M., Gustafson E.L., Borden L.A.,
RA Branchek T.A., Weinschenk R.L.;
RT "Molecular cloning of an orphan transporter. A new member of the
RT neurotransmitter transporter family.";
RL FEBS Lett. 357:86-92(1995).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE SODIUM-NEUROTRANSMITTER SYMPORTER
CC FAMILY (SNF).
DR EMBL; S76742; AAB32806.1; -.
DR InterPro; IPR000175; Na/ntran_symport.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSMPORT.
DR ProDom; PD000448; Na/ntran_symport; 2.
DR PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; FALSE_NEG.
DR PROSITE; PS00754; NA_NEUROTRAN_SYMP_2; FALSE_NEG.

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DR PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.
KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
FT Symport.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 58
FT DOMAIN 59 66 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 67 87
FT DOMAIN 88 103 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 104 124
FT DOMAIN 125 189 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 190 210
FT DOMAIN 211 239
FT TRANSMEM 219 239
FT DOMAIN 240 265
FT TRANSMEM 266 286
FT DOMAIN 287 300
FT TRANSMEM 301 321
FT DOMAIN 322 413
FT TRANSMEM 414 434
FT DOMAIN 435 455
FT TRANSMEM 456 476
FT DOMAIN 477 489
FT TRANSMEM 490 510
FT DOMAIN 511 533
FT TRANSMEM 534 554
FT DOMAIN 555 578
FT TRANSMEM 579 599
FT DOMAIN 600 616
FT CARBOHYD 155 155
FT CARBOHYD 381 381
SQ SEQUENCE 616 AA; 68971 MW; 680DAB04315CB829 CRC64;

Query Match 34.1%; Score 1302.5; DB 11; Length 616;
Best Local Similarity 43.1%; Pred. No. 5.3e-97;
Matches 265; Conservative 122; Mismatches 191; Indels 37; Gaps 14;

QY 38 LNVAGEAGGKQKAVEEELDAED----RPAWNSKLYLAQIGFSGVLGNWIRPPYLCQKN 93
DB 3 LAIKRRASRGQPGDEKRAEDMEKARQWGNPQGFVACISYAVGLGNWIRPPYLCQMY 62

QY 94 GGGAYLVYLLIIIGIPLFELEAVGQIRRGSGVWHYICPRLGIGGFSCIVCLFV 153
DB 63 GGGFLVYLLIIVGEPHLLYLEAVGQIRRGSGVWHYICPRLGIGGFSCIVCLFV 122

QY 154 GLYNVIIGWSIFVFFKFSQYPLPNSCEPVRNRSVAVVEACEKSSATTYFWRBALDI 213
DB 123 SMYINVINAWGFYLFHFSQDPLPWSVCLP--NSNRTGYDECEKASSQYFWRKTLNI 180

QY 214 SDSISESGLNWKWTLCLLVVWSIGMVGKIQSGKVMYFSSLPYVVLACFLVRGLL 273
DB 181 SPISQENGQVQWEPALCUTLAWLMVYLICILRGTESTGKVVYFTALMPYCVLIYLVRLGT 240

QY 274 LRGAVDGILHMTPTKLVKMLDPQWVREAVQVFFGLGIGFGVGVIVFSSYNKODNCHFDG 333
DB 241 LHGATNGLMYMTPKIEOLANPKAWINAATQIFSLGIGFGLSLIAFASNEPSNDCQKIA 300

QY 334 ALVSEFINFTSVLATLVVVLGFKANIMNEKCVVNAEKILGYLNTNVLRSRLDIPPHVN 393
DB 301 VIVSVINSSTISFASIVTFSYGEKATFNENCL----NKVI--LLLTN--SFDL-----E 348

QY 394 FSHLTLDYMDNDVIMTVKEDQFSA--GLDPCLEDELKSDVOGTGLAFAFTAMTH 451
DB 349 DGFTASLEKVDYLASTYPNKSEVFPNRCSELENTAVOQGTGLAFAIVYEAIAKN 408

QY 452 FPTSPPFSVMFFMLINILGLSGMIGTMAGITPIID----TSKVPKEMFTVGCCTFELV 507
DB 409 MEVSQLSVLYFFMLLMGMSMLGNTAAITPLTDSKVISSYLPKAEISGLVCLINCAV 468

QY 508 GLLFVQSGNFTVWFDDYSATPLTLTILVILENIAVNIYGPKEFQEMLEMLGRPPYRF 567
DB 469 GWFTMEAGNYWFDIFNDYATLTLTLLILVETIAVYVYVLRFPESDLRAMTG-RPLNW 527

QY 568 YF-YMWKFSVSLC--MAVLTTASTIQLGVTTPPAYSAIKKEAERYLYFPNWP---MAL 620

DB 528 YWKAWARVSPLLIIGLFIYFSLDYLITGLT--QYQAW---DATQGLVTKDYPPHALAV 582
QY 621 LITLIVATLPIPVV 635
DB 583 IGLLVASSTMCIPLV 597

RESULT 9
Q91WT6 PRELIMINARY; PRT; 635 AA.
AC Q91WT6;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
DE X transporter protein 3.
GN XTRP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013484; AAI13484.1; -.
DR MGD: MGI1336891; Xtrp3.
DR InterPro: IPR000175; Na/ntran_sympot.
DR Pfam: PF00209; SNF; 1.
DR PRODOM: PD000448; Na/ntran_sympot; 2.
DR PROSITE: PS50267; NA_NEUROTRAN_SYMP_3; 1.
SQ SEQUENCE 635 AA; 70660 MW; EC913793A807EC7B CRC64;

Query Match 34.1%; Score 1302.5; DB 11; Length 635;
Best Local Similarity 41.3%; Pred. No. 5.5e-97;
Matches 266; Conservative 132; Mismatches 197; Indels 49; Gaps 15;

QY 26 ALEPVDYKQSVLNAVAGEAG--GKQKAVE-----EELDAEDPAWNSKLYIILAQIG 75
DB 8 AVSLPEDEELQWAGGAGGPGQHPGRSTECAPGVVEKV----RPKWNPLQFLVLCITS 63

QY 76 FSVGLGNIRWPPYLCQKNGGAYLVYLLIIIGIPLFELEAVGQIRRGSGVWHYI 135
DB 64 YAVGLGNWIRPPYLCQMYGGSGFLVPIIIMLIVEGMPLLYLEAVGQIRRGSGVWHYI 123

QY 136 CPRLGIGGFSCIVCLFVGLIYVNIIGWSIFVFFKFSQYPLPNSCEPVRNRSVAVVEAE 195
DB 124 SPYLSGVGIAVLVVSFLASVYFNVNTWALWYLFHFSQDPLPWSVCLP--NSNHTGYDEE 181

QY 196 CEKSSATTYFWRREALDISDSISGGLNWKWTLCLLVVWSIGMVGKIQSGKVMYF 255
DB 182 CERASSQYFWRKTLNISPISQENGQVQWEPALCUTLAWLMVYLICILRGTESTGKVVYF 241

QY 256 SSFLPPYVLACFLVRGLLRRGAVDGIHMTPTKLVKMLDPQWVREAVQVFFGLGFGG 315
DB 242 TTSLPYFVLIYLVRLGLTHGATNGLAYMTPKIEOLANPKAWINAATQIFSLGIGCGG 301

QY 316 VIVFSSYNKODNCHFDGALVSFINFTSVLATLVVVLGFKANIMNEKCVVNAEKIL 375
DB 302 LIAFASNEPSNDCQKIALIVSVINSTTAIFSSIVTFSYGEKATFNENCL----NKVI 357

QY 376 GYLNTNVLRSRLDIPPHVNFSLHTTKDYMDNDVIMTVKEDQFSA--GLDPCLEDELK 433
DB 358 -LLLTN--SFDL-----EDGFLTVSNLEEVKNLASTYPNKSEVFPNRCSELENT 409

QY 434 SVQGTGLAFAFTAMTHFTSPSPFWSNVFFMLINILGLSGMIGTMAGITPIID----TS 489
DB 410 AVQGTGLAFAIVYEAIAKNMEVSQLSVLYFFMLLTGMSVMVGTGTAITPLTDSKI 469

QY 490 KVPKEMFTVGCCTFELVGLLFLVQSGNFTVWFDDYSATPLTLTILVILENIAVNIYGP 549
DB 470 YLPKAEISGLVCLINCAVIGWFTMEAGNYWFDIFNDYATLTLTLLILVETIAVYVYGL 529

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QY 550 KKFQELTEMLGFRPYRFFYFWMKFSVPLCMA---VLTASIIQLGVTTPPAYSAWIKEA 606
DB 530 KRFSDLRAMTGRSLTSWTKVMWAEVSPLLIVGLFIFYLSYLTGTL--QYQAW---DA 584

QY 607 AERYLY---FPNWPMLLITLVATLPVPV---FVLRHFHL 643
DB 585 TOGHVTKDYPTALAVIGLLVASSTMCIPALGTFVTRHFKI 628

RESULT 10
O88575 ID O88575 PRELIMINARY; PRT; 635 AA.
AC O88575;
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Sodium- and chloride-dependent transporter XTRP3.
GN XTRP3 OR XT3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[.]
RN SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=KIDNEY;
RX MEDLINE=99131080; PubMed=9932288;
RA Nash S.R., Giros B., Kingsmore S.F., Kim K.M., El-Mestikawy S.,
RA Dong Q., Fumagalli F., Seldin M.F., Caron M.G.;
RT "Cloning, gene structure, and genomic localization of an orphan
RT transporter from mouse kidney with six alternatively-spliced
RT isoforms."
RL Recept. Channels 6:113-128(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: KIDNEY.
CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
CC FAMILY (SNF).
DR EMBL; AF075261; AAC27756.1; -.
DR MGD; MGI:1336891; Xtrp3.
DR InterPro; IPR000175; Na/ntran_symport.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSMPORT.
DR PRODOM; PD000448; Na/ntran_symport; 2. FALSE_NEG.
DR PROSITE; PS00610; NA_NEUROTRAN_SYMPT_1; FALSE_NEG.
DR PROSITE; PS00754; NA_NEUROTRAN_SYMPT_2; FALSE_NEG.
DR PROSITE; PS0267; NA_NEUROTRAN_SYMPT_3; 1.
KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
KW Symport.
FT DOMAIN 1 56 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 57 77 1 (POTENTIAL).
FT DOMAIN 78 85 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 86 106 2 (POTENTIAL).
FT DOMAIN 107 127 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 128 148 3 (POTENTIAL).
FT DOMAIN 149 208 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 209 229 4 (POTENTIAL).
FT DOMAIN 230 237 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 238 258 5 (POTENTIAL).
FT DOMAIN 259 284 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 285 305 6 (POTENTIAL).
FT DOMAIN 306 319 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 320 340 7 (POTENTIAL).
FT DOMAIN 341 432 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 433 453 8 (POTENTIAL).
FT DOMAIN 454 474 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 475 495 9 (POTENTIAL).
FT DOMAIN 496 508 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 509 529 10 (POTENTIAL).
FT DOMAIN 530 547 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 548 568 11 (POTENTIAL).
FT DOMAIN 569 597 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 598 618 12 (POTENTIAL).
FT DOMAIN 619 635 CYTOPLASMIC (POTENTIAL).

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FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 635 AA; 70641 MW; EC9272C12507EC7B CRC64;

Query Match 34.1%; Score 1300.5; DB 11; Length 635;
Best Local Similarity 41.3%; Pred. No. 8e-97;
Matches 266; Conservative 131; Mismatches 198; Indels 49; Gaps 15;

QY 26 ALEEPVDYKQSVNLVAGEAG---GKQAVE-----EELDAEDRPANWSKLYLAQIG 75
DB 8 AVSLFEDEDELQWGGAGGQHPGRPRSTECAPGVVKEV---RPNWNLQFLLVCS 63

QY 76 FSVGLGNWRFPYLCOKNGGAYLYPVYLVLLIIGIPLEFLELAVGORIRGSGVWYI 135
DB 64 YAVGLGNWRFPYLCOMYGGSFLVYIIMLIVEGMLLYLELAVGORMRAGSGAWRTI 123

QY 136 CPRLGGICFSSCTVCLFVGLYNYVIIGWSIFYPFKFSQYPLPWSECPVVRNGSVAAVE 195
DB 124 SPYLSGVGIASLVSVFLASVIFNVNTWALWYLFHSQDPLPWSVCLP--NSNHTGYDEE 181

QY 196 CEKSSATYFWYREALDISSESGLNKNKMTLCLLVWVSIGGMVAGKGIQSSKVMYF 255
DB 182 CEKASSTQYFWYRKTNLNPSIQENGSGVQWEPALCLTLAWLMVYLILRGTESTGKVVYF 241

QY 256 SSLFPYVVLACFLVRGLLRLGAVDGLHMETPKLYKMLDPQVWREVAQVFGGLGEGG 315
DB 242 TTSLPYFVLIYLVRLTLHGATNGLAYMETPKIEQLANPKAWINAAQIFSLGLGCGG 301

QY 316 VIVFSSYNKODNCHDFGALVSFINFTSVLATLVVFLGFKANIMKEKCVVENAEKIL 375
DB 302 LIAFASYNPSNDCQKHALIVSNSTAFSSIVTSIYGFKATFNENCL---NKVI 357

QY 376 GYLNTNVLSDRLIPPHVNSHLTKDYEMDNVIMTWKEDQFSAL--GLDPCLLDELDK 433
DB 358 -LLLTN--SFDL-----EDGFLTVSNLEEVKNVLAITYSEVFPNIRNGSLELDT 409

QY 434 SVQGTGLAFTAFTEAMTHPTSPFSVWFFLNLGLSGMGTWAGTTTPIID---TS 489
DB 410 AVQGTGLAFIVYTEAKNMEVSQVLSVLYFMLTLGLMGSMVGGTALTPLTDSKIIS 469

QY 490 KVPKEMFTGCCVFTFLVGLLFVQRSGNYFVTMEDDYSATLPLTLIVILENTAVAWIYGP 549
DB 470 YLPKEAISGLVCLLNCAIGMVTMEAGNWFEDLNDYTATLSLLILVILENTAVACVYGL 529

QY 550 KKFQELTEMLGFRPYRFFYFWMKFSVPLCMA---VLTASIIQLGVTTPPAYSAWIKEA 606
DB 530 KRFSDLRAMTGRSLTSWTKVMWAEVSPLLIVGLFIFYLSYLTGTL--QYQAW---DA 584

QY 607 AERYLY---FPNWPMLLITLVATLPVPV---FVLRHFHL 643
DB 585 TOGHVTKDYPTALAVIGLLVASSTMCIPALGTFVTRHFKI 628

RESULT 11
Q62687 ID Q62687 PRELIMINARY; PRT; 615 AA.
AC Q62687;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Renal osmotic stress-induced Na-cl organic solute cotransporter.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[.]
RN SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY CORTEX;
RX MEDLINE=95029937; PubMed=7943364;
RA Wasserman J.C., Delpire E., Tonidandel W., Kojima R., Gullans S.R.;
RT "Molecular characterization of ROSIT, a renal osmotic stress-induced
RT Na(+)-Cl(-)-organic solute cotransporter."
RT Am. J. Physiol. 267:F688-F694(1994).

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DR EMBL; U12973; AAC13771.1; -
DR InterPro; IPR000175; Na/ntran_sympoort.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSPORT.
DR PROSITE; PD000448; Na/ntran_sympoort; 2.
DR PROSITE; PS0267; NA_NEUROTRAN_SYMP_3; 1.
SQ SEQUENCE 615 AA; 69556 MW; F41E7DE1DC276918 CRC64;

Query Match 33.9%; Score 1294.5; DB 11; Length 615;
Best Local Similarity 42.0%; Pred. No. 2.4e-96;
Matches 253; Conservative 121; Mismatches 189; Indels 39; Gaps 10;

QY 43 BAGGQKAVEBELDAEDRPANMSKQYILAQIGFSGVLGNIRFPYLCQKNGGAGLVIPY 102
Db 3 QASGMDPLVDIE---DERPKWKNQYLLSCIGFAVGLGNIRFPYLCCHTGGGAFIPY 59
QY 103 LVLLIIIGIPFFLELAVGORIRRSIGVWHYICPRGLGIGSSCIVCLFVGLYYNIIG 162
Db 60 FIALVFEGIPFLYELAIQORLRSGISGVWKTISPYLGGVGLGCFVSFLVSLYYNTILL 119
QY 163 WSIFFFKSFQVPLPWSCEPVVRNGSVAVAECEKSSATTYFWYREALDISDSISESG 222
Db 120 WVLWFELNSFOHLPWSTCPLDNLRTGFV--QECQSSGTVSFYRWQTLNITSDISNTGT 177
QY 223 LNWMTCLLVVWSIGGNAVKGIOSSGKVMYFSSLPYVVLACFLVRLGLLRGAVDGL 282
Db 178 IQWLFLCLVACVTTVYLCVIRGIESTGKVIYFTALFPYLVLTIFLIRGLTLPGATEGLT 237
QY 283 HMEYTPKLVKMLDPQVWREVATQVFFGLGFGGVIVFSSYNKQDNNCHDFDGLVSVINFF 342
Db 238 YLFTPNMKILQNSRVMLDAAQIIFPSLSLAFGGHIAFASYNQPRNCKEADATIALVNSM 297
QY 343 TSVLATLVVYVVLGFKANIMEKCVVENAEKILGYLNTNVLNLSKRLIPPHVNFSLT-TKD 401
Db 298 TSLVASTITFISMGFKASNDYGRCLDRN--ILSLIN-----EFDFPELSISRD 343
QY 402 YNEMDNVIM---TVKEDQFSAIGLDPCLLEDELKSVQGTGLAFIATFAMTHFTSPFW 458
Db 344 --EYPSVLMYLNATQPERVALPLKTHLEDPLDFLSASGPGIAFIVFTEAVLHMPGASVW 401
QY 459 SVMFFMLINILGLSGMIGTMAITPIID---TSKVPKEMFTVGCCTFELVGLLVFOR 514
Db 402 SVLFEGMLFTLGLSSMFMNGEVITPLFDMGLPKGVKFEKMTGVVCFCLFSAICFTIQ 461
QY 515 SGNTFVTMFDYSATPLTLIVILENIAVMIYGPKKFQMOELTEMLGFRPYRFFYMWKF 574
Db 462 SGSYWLEIFDSFAASNLIIIFAFMEVGVVHYGKRCDDIEWMTGRRPSLYWQVTVRW 521
QY 575 VSPCLMAVLTASIIOLGVTTPPAYSAWIKKEAERYLYPPN-----WPMALLITLIVAT 629
Db 522 VSPMLLFGIFUSYIVLLAQSSPSYKAW-----NPQYEHFPPSREKLYPGWVQVTCVLLSF 576
QY 630 LP 631
Db 577 LP 578

RESULT 12
Q96N87
ID Q96N87 PRELIMINARY; PRT; 628 AA.
AC Q96N87;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CDNA FLJ1236 fis, clone KIDNE2004828, moderately similar to Mus
DE musculus orphan transporter isoform A12 (Xtrp2) mRNA.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
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RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine K., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.,
KT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK055798; BAB71018.1; -
DR InterPro; IPR000175; Na/ntran_sympoort.
DR Pfam; PF00209; SNF; 1.
DR PROSITE; PD000448; Na/ntran_sympoort; 2.
DR PROSITE; PS0267; NA_NEUROTRAN_SYMP_3; 1.
SQ SEQUENCE 628 AA; 70924 MW; 90EA71CD12C6DC9D CRC64;

Query Match 33.6%; Score 1282; DB 4; Length 628;
Best Local Similarity 42.2%; Pred. No. 2.5e-95;
Matches 251; Conservative 111; Mismatches 189; Indels 44; Gaps 10;

QY 58 EDRPAWNSKIQYILAQIGFSGVLGNIRFPYLCQKNGGAYLVPLVLLIIGIPFFLE 117
Db 16 DERPKWKNQYLLSCIGFAVGLGNIRFPYLCQYGGAFIPYVIALVFFEGIPFHV 75
QY 118 LAVGORIRRSIGVWHYICPRGLGIGSSCIVCLFVGLYYNIIGSYFIFKSFQYPLP 177
Db 76 LAIQORLRKSGVGYWTAISPYSVLGVCVLSFISLYNTIVAWLWILNLSPOHPLP 135
QY 178 WSECP--VVRNGSVAVVAEACEKSSATTYFWYREALDISDSISESGLNKRWKTLCLVVM 235
Db 136 WSSCPPDLNRTGFV---EECGSSAVSYFWYQTLNITADINDSSIQWLLICLAASM 191
QY 236 SIGMAYGKGTQSSGKVMYFSSLPYVVLACFLVRLGLLRGAVDGLHMTFPLVKMLDP 295
Db 192 AVVMCMVIRGIETTKVIYFTALFPYLVLTIFLIRGLTLPGATKGLIYLTENMHILQP 251
QY 296 QVWREVATQVFFGLGFGGVIVFSSYNKQDNNCHDFDGLVSVINFFTSVLTATLVVFFVL 355
Db 252 RVMLDAAQIIFPSLSLAFGGHIAFASYNPRNCKOQDAVIALVNRMTSLYASIAVSVL 311
QY 356 GFRANIMNEKCVVENAEKILGYLN-----TNVLSRDLIPP---HVNFSHLTKDYMEMDN 407
Db 312 GFRATNDEYHCLDRN---ILSLINDFDPQESIRDDYPVLMHLN----- 354
QY 408 VIMTVKEDQFSAIGLDPCLLEDELKSVQGTGLAFIATFAMTHFTSPFWVSMFPLMLI 467
Db 355 ---ATWPKRVAQLPKACLEDFLDKKSASGPGIAFVETETDLHMPGAPVWMLFFGMLP 411
QY 468 NLGLSGMIGTMAITPIIDTSK---VPKEMFTVGCCTFELVGLLFVORSGNYFVTMF 523
Db 412 TLGLSTWFTGVEAVITPLLDVGVLPWVVPKREALTGLVCLVCLFSATCTFLOSGNYWLEIF 471
QY 524 DDYSATPLTLIVILENIAVMIYGPKKFQMOELTEMLGFRPYRFFYMWKFSPLCMAYL 583
Db 472 DNFAASNLMLLAFLEVVGVVYVYCMKRCDDIAMTGRPPSYWRLTWRVSPILLTIF 531
QY 584 TTASIIOLGVTTPPAYSAWIKKEAERYLYPPN-----EAAERYLYPPNPMALLITLIVATLPIV 634
Db 532 -VAVIILLFWKPLRYKAWNPAYELPPSQEKLY-PGWARAACVLLSLVLPWVPV 584

RESULT 13
Q91XG6
ID Q91XG6 PRELIMINARY; PRT; 577 AA.
AC Q91XG6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to X transporter protein 2.
GN XTRP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```



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RESULT 15
Q9BYZ7
ID Q9BYZ7 PRELIMINARY; PRT; 397 AA.
AC Q9BYZ7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Sodium channel-like protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Londono-Vallejo J.A.;
RT "Sequence of a BAC carrying the entire hTERT gene.";
RL Submitted (Sep-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY007685; AAG23290.1; -.
DR InterPro; IPR00175; Na/ntran_sympot.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSMPORT.
DR PRODOM; PD000448; Na/ntran_sympot; 1.
DR PROSITE; PS0267; NA_NEUOTRAN_SYMP_3; 1.
SQ SEQUENCE 397 AA; 43784 MW; E70588E4D7FD9CF6 CRC64;

Query Match 26.8%; Score 1024; DB 4; Length 397;
Best Local Similarity 38.18; Pred. No. 1.le-74;
Matches 189; Conservative 87; Mismatches 104; Indels 116; Gaps 5;

QY 58 EDPAWNSKLOYILAQIGFVGLGNIRFPYLCQKNGGAYLVPLYLVLLIIGIPFFLE 117
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 16 DERPKWNKAQYLLSCIGFAVGLGNIRFPYLCQYGGAFLLPYVIALVFEIGIPFHE 75

QY 118 LAVQQRIRRGISGVWHYICPRLLGGIGFSSCIVCLFVGLYVYVNIIGWSIPYFKSQYPLP 177
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 76 LAIGQRLKRGVGVWTAISPLYLSGVLGCVTLISFLISLYNTIVAVWVLLNSFQHP 135

QY 178 WSECP--VVRNGSVAVVEACEKSAITYFWYREALIDISDSISEGGLNWKMTLCLLVWV 235
   |||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 136 WSSCFPDLNRGFGV----EEQGSASVSYFWYRQTLNITADINDSGSIQWLLICLAASW 191

QY 236 SIGGMVKGKIQSSGKVMYFSSLPFYVVLACPLVRGLLRGAVDGLHMTPKLVKMLDP 295
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 192 AVVYMCVIRGIEETGKVYFTALFPYLVLTIFLRGLTLPGATKGLIYLFTEP-----NP 246

QY 296 QVREVAQVFEGLGFGGVIVFSSYNKQDNCHDFGALVSFINFFTSVLTATLVVFFVL 355
   |||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 247 RVLDAATQIFESLSLAEGGHIAFASVNSPRNDCOKDAVIALVNRMTSLYASIAVFSVL 306

QY 356 GFKANIMNEKCVVENAEXILGYLNTNVLRSDLIPPHVNFSLTTKDYMEMDNVIMTVKED 415
   |
Db 307 G-----307

QY 416 QFSALGLDPCLEDELDSVOGTGLAFIAFTAEAMTHFTSPFWSVWFFLMLINLGLGSMI 475
   |||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 308 -----ASQPGLAFAVVFETETDLHMPGAPVWAMLFPGMLFTLGLSTMF 348

QY 476 GTMAGITPPIIDTSKVPKEMTVGCCVFTFLVGLLFVQBSGNGYFVTMFDYSATLPLTLI 535
   |||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 349 GTVEAVITPLLD-----SGNIWLEIFDNFAASLNLML 381

QY 536 VILENIAVAVIYGPKK 551
   || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 382 AFLEWGVVYVYGMKR 397
```

Search completed: April 21, 2003, 13:57:45
Job time : 101 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 13:46:57 ; Search time 27 seconds
(without alignments)
1116.789 Million cell updates/sec

Title: US-09-923-444A-2
Perfect score: 3817
Sequence: 1 MPKNSKVTQREHSEHVYES.....NPNPGYGRGYLLASTPESEL 727

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3610	94.6	727	1 NTH4_RAT	P31662 rattus norv
2	2522.5	66.1	730	1 NTH7_HUMAN	Q9HJ77 homo sapien
3	2494	65.3	729	1 NTH7_BOVIN	Q9XS59 bos taurus
4	2488	65.2	729	1 NTH7_RAT	Q08469 rattus norv
5	2184	57.2	439	1 NTH4_HUMAN	Q9HJ48 homo sapien
6	1147	30.0	235	1 NTH4_BOVIN	Q28001 bos taurus
7	1134	29.7	736	1 NTH5_HUMAN	Q9GZ46 homo sapien
8	1036.5	27.2	797	1 S6A5_HUMAN	Q9Y345 homo sapien
9	1028	26.9	799	1 S6A5_RAT	P58295 rattus norv
10	1004	26.3	633	1 S6A9_RAT	P28572 rattus norv
11	995.5	26.1	692	1 S6A9_HUMAN	P48067 homo sapien
12	985.5	25.8	617	1 S6A2_HUMAN	P23975 homo sapien
13	985.5	25.8	638	1 S6A3_BOVIN	Q28039 bos taurus
14	981.5	25.7	619	1 S6A3_RAT	P23977 rattus norv
15	981.5	25.7	633	1 S6A9_MOUSE	P28571 mus musculu
16	976.5	25.6	619	1 S6A3_MOUSE	Q61327 mus musculu
17	975.5	25.6	617	1 S6A2_MOUSE	Q55192 mus musculu
18	974.5	25.5	635	1 S6A8_RAT	P28570 rattus norv
19	969.5	25.4	614	1 S6AC_RAT	P48056 rattus norv
20	969.5	25.4	635	1 S6A8_RABIT	P31661 oryctolagus
21	968.5	25.4	614	1 S6AC_CANFA	P27799 canis fami
22	968.5	25.4	636	1 S6A7_HUMAN	Q99884 homo sapien
23	966.5	25.3	599	1 S6A1_RAT	P23978 rattus norv
24	965.5	25.3	620	1 S6A3_HUMAN	Q01959 homo sapien
25	964.5	25.3	620	1 S6A5_BOVIN	Q9MZ34 bos taurus
26	963.5	25.2	635	1 S6A8_BOVIN	Q18875 bos taurus
27	963.5	25.2	637	1 S6A7_RAT	P28573 rattus norv
28	963	25.2	635	1 S6A8_HUMAN	P48029 homo sapien
29	962.5	25.2	615	1 S6A2_BOVIN	P51143 bos taurus
30	958.5	25.1	614	1 S6AC_RABIT	P48055 oryctolagus
31	955	25.0	614	1 S6AC_HUMAN	P48065 homo sapien
32	951.5	24.9	599	1 S6A1_HUMAN	P30531 homo sapien
33	951.5	24.9	620	1 S6A6_HUMAN	P31641 homo sapien

34	951	24.9	602	1 S6AD_MOUSE	P31649 mus musculu
35	951	24.9	602	1 S6AD_RAT	P31646 rattus norv
36	948.5	24.8	614	1 S6AC_MOUSE	P31651 mus musculu
37	947.5	24.8	630	1 S6A4_CAVPO	Q35999 cavia porce
38	946.5	24.8	630	1 S6A4_MOUSE	Q60857 mus musculu
39	946	24.8	598	1 S6A1_MOUSE	P48057 mus cookii
40	943.5	24.7	630	1 S6A4_RAT	P31652 rattus norv
41	941.5	24.7	620	1 S6A6_CANFA	Q00589 canis fami
42	941.5	24.7	630	1 S6A4_MACMU	Q9MYX0 macaca mula
43	937.5	24.6	630	1 S6A4_HUMAN	P31645 homo sapien
44	937	24.5	693	1 S6A3_BOVIN	P27922 bos taurus
45	925.5	24.2	621	1 S6A6_RAT	P31643 rattus norv

ALIGNMENTS

RESULT 1
NTT4_RAT
ID NTT4_RAT STANDARD; PRT; 727 AA.
AC P31662:
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Orphan sodium- and chloride-dependent neurotransmitter transporter
DE NTT4.
GN NTT4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93114444; PubMed=8093354;
RA Liu Q.-R., Mandiyan S., Lopez-Corcuera B., Nelson H., Nelson N.;
RT "A rat brain cDNA encoding the neurotransmitter transporter with an
RT unusual structure.";
RL FEBS Lett. 315:114-118(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94125086; PubMed=8294906;
RA el Mestikawy S., Glos B., Pohl M., Hamon M., Kingsmore S.F.,
RA Seldin M.F., Caron M.G.;
RT "Characterization of an atypical member of the Na+/Cl(-)-dependent
RT transporter family: chromosomal localization and distribution in
RT GABAergic and glutamatergic neurons in the rat brain.";
RL J. Neurochem. 62:445-455(1994).
CC -!- FUNCTION: NOT YET KNOWN, ORPHAN TRANSPORTER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CENTRAL NERVOUS
CC SYSTEM AND IS MORE ABUNDANT IN THE CEREBELLUM AND THE CEREBRAL
CC CORTEX.
CC -!- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
CC FAMILY (SNF).
CC
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CC
CC EMBL; L06434; AAB24776.1; -;
CC EMBL; S68944; AAC60673.1; -;
CC PIR; S27043; S27043.
CC InterPro; IPR000175; Na/ntran_symport.
CC Pfam; PF00209; SNF; 1.
CC PRINTS; PR00176; NANEUSMPORT.
CC ProDom; PD000448; Na/ntran_symport; 2.
CC PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; 1.
CC PROSITE; PS00754; NA_NEUROTRAN_SYMP_2; 1.


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Db 177 LPWOCPLVKNASHTFVBPCEKSSATYYWYREALNISTISSESGLNKMTICLLAAW 236
Qy 236 SIGGNVAGKQIOSSKVMYFSSLPVYLACFLVRLGALLRGAYDGLHMFPPKLVKMLDP 295
Db 237 VVVCCLAMIKIGQSSKIMYFSSLPVYLACFLVRLGALLRGAYDGLHMFPPKLVKMLDP 296
Qy 296 QVWREAVATQVFFGLGFGGVIVFSSYNKQDNCHFDGALVSNFETSVLALIVVFFVL 355
Db 297 KWREAAQVFFALGFGGVIVFSSYNKQDNCHFDGALVSNFETSVLALIVVFFVL 356
Qy 356 GFKANIMKECVENAEKILGYLNTNVLSDRLIPPHVNFSLTKDKYMDMNDVIMTKED 415
Db 357 GFKANVINEKCIASEMELIKLVKWNISQDIIPHINFSAITAEDYDLIYDIQKVEE 416
Qy 416 QFSALGLDPCLEDELDKSVQGTGLAFIAFTAMTHPTSPFWSVMFFMLNLGLGSMI 475
Db 417 EFPALHLNACQIEDELNAVQGTGLAFIAFTAMTHPTSPFWSVMFFMLNLGLGSMI 476
Qy 476 GTMAGITTPIDTSKVPKEMFTVGCCTFLVGLLVEQSGNVEFVIMFDDYSATPLTLI 535
Db 477 GTIEGIITPVVDTFKVRKEILTVICCLAFICGLIEVQSGNVEFVIMFDDYSATPLTLI 536
Qy 536 VILENIAVAVIYGPCKFMOELTEMLGFRPYFVYFMKFSVPLCMVLTITASIIQLGVP 595
Db 537 VILENIAVSVYVYIDKFMEDLMDLGTENRYYYMMKYISPLMLLSLLASIVNGLGSP 596
Qy 596 PAYSANIKKEAARYLYFPNPMALLITLIVVATLPVIVVFLRHPHLLSDGS-NLTSVS 654
Db 597 PGYNAMWEDKASEKESLYPTMGWICISLMLAILPVPVFIIRCNLIDSSGNLASVT 656
Qy 655 YKARMMKDISLEENDETRFILSKVPSEAPSPMTHRSVLGPGSPLTSNPNPGPYG 714
Db 657 YKRGVLKEPVNL-EGDDASLHGKISSESSPFGKNIRYKQSGSPTLDTA--PNRGY 713
Qy 715 RGYLLA---STPESEL 727
Db 714 IGYLMADMPDESGL 729

RESULT 4
NTT7_RAT
ID NTT7_RAT STANDARD; PRT: 729 AA.
AC Q08469; Q63838;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Orphan sodium- and chloride-dependent neurotransmitter transporter
DE NTT73 (Orphan transporter v7-3).
GN NTT73.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93180651; PubMed=1363329;
RA Uhl G.R., Kitayama S., Gregor P., Nanthakumar E., Persico A.M.,
RA Shimada S.
RT "Neurotransmitter transporter family cDNAs in a rat midbrain library:
RL 'orphan transporters' suggest sizable structural variations.";
RL Brain Res. Mol. Brain Res. 16:353-359(1992).
CC -1- FUNCTION: NOT YET KNOWN, ORPHAN TRANSPORTER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
CC FAMILY (SNF).
CC -----
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CC -----
DR EMBL; L22022; AAA41729.1; -.
DR EMBL; S5968; AAB25532.1; -.
DR InterPro; IPR000175; Na/ntran_symport.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSMPORT.
DR ProDom; PD000448; Na/ntran_symport; 2.
DR PROSITE; PS00610; NA_NEUROTRAN_SYMPT_1; 1.
DR PROSITE; PS00754; NA_NEUROTRAN_SYMPT_2; FALSE_NEG.
DR PROSITE; PS0267; NA_NEUROTRAN_SYMPT_3; 1.
KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
KW Symport.
FT DOMAIN 1 69 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 70 90 1 (POTENTIAL).
FT TRANSMEM 98 117 2 (POTENTIAL).
FT TRANSMEM 142 162 3 (POTENTIAL).
FT DOMAIN 163 225 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 226 244 4 (POTENTIAL).
FT TRANSMEM 253 270 5 (POTENTIAL).
FT TRANSMEM 306 323 6 (POTENTIAL).
FT TRANSMEM 335 356 7 (POTENTIAL).
FT DOMAIN 357 452 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 453 472 8 (POTENTIAL).
FT TRANSMEM 496 514 9 (POTENTIAL).
FT TRANSMEM 530 550 10 (POTENTIAL).
FT TRANSMEM 571 592 11 (POTENTIAL).
FT TRANSMEM 620 642 12 (POTENTIAL).
FT DOMAIN 643 729 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 383 383 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 1 3 MPK -> IP (IN REF. 1; AAB25532).
SQ SEQUENCE 729 AA; 81596 MW; ECDDC6403741B53E CRC64;

Query Match 65.2%; Score 2488; DB 1; Length 729;
Best Local Similarity 63.9%; Pred. No. 1.5e-155;
Matches 473; Conservative 109; Mismatches 134; Indels 24; Gaps 8;

Qy 1 MPKNSKVTQREHSEHVESVADLLALEPVD--YKOSVLNVAGBAGKQKAVEELDAE 58
Db 1 MPKNSKVKVRD-LDDVDVIESVKLLSNEDSVEDYSKSELIVDQV-----T-EKDTDAE 52
Qy 59: D-----RPANNSKLYILAQIGFSVGLGNWIRFPYLCQKNGGAYLVPLVLLIIGI 111
Db 53 DGEVDDERPAWNSKLYILAQIGFSVGLGNWIRFPYLCQKNGGAYLVPLVLLIIGI 112
Qy 112 PLFLELAVGQIRIRGSGVWVHYICPLGGIGFSSCIVCLFVGLYVNVYIIGHSIFVFKS 171
Db 113 PLFLELAVGQIRIRGSGVWVHYISPKLGGIGFASCVVYFVALYVNVYIIGHTLFFYSQS 172
Qy 172 FOYPLPWSCEPVRNGSVAVVEACEKSSATYYFYREALDISDSISSESGLNKMTICL 231
Db 173 FOQPLPWQCPLVKNASHTYIEPECEKSSATYYFYREALAISSESSISSESGLNKMTICL 232
Qy 232 LVVWSITGGMAVKGIOSSKVMYFSSLPVYLACFLVRLGALLRGAYDGLHMFPPKLVK 291
Db 233 LAAMVVCAMIKIGQSSKIMYFSSLPVYLACFLVRLGALLRGAYDGLHMFPPKLVK 292
Qy 292 MLDPOVWREAVATQVFFGLGFGGVIVFSSYNKQDNCHFDGALVSNFETSVLALIVV 351
Db 293 MLEPKVWREAVATQVFFALGFGGVIVFSSYNKQDNCHFDGALVSNFETSVLALIVV 352
Qy 352 FVVLGFKANIMKCVVENAEKILGYLNTNVLSDRLIPPHVNFSLTKDKYMDMNDVIMTK 411
Db 353 FAVLGFKANIVNEKCIASEMELIKLVKWNISQDIIPHINFSAITAEDYDLIYDIQK 412
Qy 412 VKEDQFSALGLDPCLEDELDKSVQGTGLAFIAFTAMTHPTSPFWSVMFFMLNLGL 471
Db 413 VKEEEFAVLHLKACQIEDELNAVQGTGLAFIAFTAMTHPTSPFWSVMFFMLNLGL 472
Qy 472 GSMIGTMAGITTPIDTSKVPKEMFTVGCCTFLVGLLVEQSGNVEFVIMFDDYSATPL 531
Db 473 GSMIGTMAGITTPIDTSKVPKEMFTVGCCTFLVGLLVEQSGNVEFVIMFDDYSATPL 532
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DR EMBL; U19593; AAA61578.1; -.
DR InterPro; IPR000175; Na/ntran_sympot.
DR Pfam; PF00209; SNF; 1.
DR ProDom; PD000448; Na/ntran_sympot; 1.
DR PROSITE; PS00610; NA-NEUROTRAN_SYMP_1; 1.
DR PROSITE; PS00754; NA-NEUROTRAN_SYMP_2; 1.
DR PROSITE; PS0267; NA-NEUROTRAN_SYMP_3; 1.
KW Neurotransmitter transport; Transmembrane; Glycoprotein;
KW Sympt.
FT NON_TER 1 1 (POTENTIAL).
FT TRANSMEM <1 8
FT TRANSMEM 16 35
FT TRANSMEM 60 80
FT DOMAIN 81 143 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 162 4 (POTENTIAL).
FT TRANSMEM 171 188 5 (POTENTIAL).
FT TRANSMEM 224 >225 6 (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC.. ) (POTENTIAL).
FT NON_TER 225 225
SQ SEQUENCE 225 AA; 25374 MW; 3FA15D33F76D15C3 CRC64;

Query Match 30.0%; Score 1147; DB 1; Length 225;
Best Local Similarity 93.8%; Pred. No. 2.3e-68;
Matches 211; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 82 NIWRPFLCQKNGGGAYLPVLLIIIGIPFLFLEAVGQIRRGSGVWVHYICPRLGG 141
D 1 NIWRPFLCQKNGGGAYLPVLLIIIGIPFLFLEAVGQIRRGSGVWVHYICPRLGG 60
QY 142 IGFSSICVCLFVGLYNYVIGWSIFEFKSFQYPLPWSCEPVVRNGSVAVVEACEKSSA 201
D 61 IGFSSICVCLFVGLYNYVIGWSIFEFKSFQYPLPWSCEPVVRNGSVAVVEACEKSSA 120
QY 202 TTYFYREALDISDSSESGGLNWKMTCLLLVYVMSIGGMVAVGKIQSGKVMYFSSLPFY 261
D 121 TTYFYREALDISDSSESGGLNWKMTCLLLVAVRIVGMVAVRGIQSGKVMYFSSLPFY 180
QY 262 VYLACFLVRLGRLRGAVDGLHMFTEPKLVKMLDPQVWREVATQVF 306
D 181 VYLACFLVRLGRLRGAVDGLHMFTEPKLVKMLDPQVWREVATQVF 225

RESULT 7
NTT5_HUMAN STANDARD; PRT; 736 AA.
ID NTT5_HUMAN
AC Q9GZ6; Q9Y519;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Orphan sodium- and chloride-dependent neurotransmitter transporter
DE NTT5.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Testis;
RA Sloan J.L., Mager S.;
RT "Cloning of a new member of the neurotransmitter transporter family.";
RL Abstr. - Soc. Neurosci. 24:1606-1606(1998).
[2]
SEQUENCE FROM N.A.
TISSUE=Testis;
RX Farmer M.K., Robbins M.J., Medhurst A.D., Campbell D.A., Ellington K.,
RA Duckworth M., Brown A.M., Middlemiss D.N., Price G.W., Pangalos M.N.;
RT "Cloning and characterization of human NTT5 and v7-3; two orphan
RT transporters of the Na(+)/Cl(-)-dependent neurotransmitter
RT transporter gene family.";
RL Genomics 70:241-252(2000).
[3]

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RP SEQUENCE FROM N.A.
RX TISSUE=Testis;
RX MEDLINE=21154917; PubMed=11230166;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansong W., Boecher M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Newes H.-W., Ottenwaeider B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Pousta A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435(2001).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in peripheral tissues,
CC particularly in testis, pancreas, and prostate.
CC -!- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
CC FAMILY (SNF).
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CC
DR EMBL; AF151977; AAD38044.1; -.
DR EMBL; AF265578; AAG41362.1; -.
DR EMBL; AL136856; CAB66790.1; -.
DR InterPro; IPR000175; Na/ntran_sympot.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUMPORT.
DR ProDom; PD000448; Na/ntran_sympot; 2.
DR PROSITE; PS00610; NA-NEUROTRAN_SYMP_1; FALSE_NEG.
DR PROSITE; PS00754; NA-NEUROTRAN_SYMP_2; FALSE_NEG.
DR PROSITE; PS0267; NA-NEUROTRAN_SYMP_3; 1.
KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
KW Sympt.
FT DOMAIN 1 138 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 139 159 1 (POTENTIAL).
FT TRANSMEM 177 197 2 (POTENTIAL).
FT TRANSMEM 199 219 3 (POTENTIAL).
FT DOMAIN 220 263 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 264 284 4 (POTENTIAL).
FT TRANSMEM 290 310 5 (POTENTIAL).
FT TRANSMEM 338 358 6 (POTENTIAL).
FT TRANSMEM 383 403 7 (POTENTIAL).
FT DOMAIN 404 495 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 496 516 8 (POTENTIAL).
FT TRANSMEM 534 554 9 (POTENTIAL).
FT TRANSMEM 568 588 10 (POTENTIAL).
FT TRANSMEM 609 629 11 (POTENTIAL).
FT TRANSMEM 659 679 12 (POTENTIAL).
FT DOMAIN 680 736 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 229 229 N-LINKED (GLCNAC.. ) (POTENTIAL).
FT CONFLICT 181 181 W -> R (IN REF. 1).
FT CONFLICT 307 307 W -> GG (IN REF. 1).
SQ SEQUENCE 736 AA; 82199 MW; E21EA16515446C35 CRC64;

Query Match 29.7%; Score 1134; DB 1; Length 736;
Best Local Similarity 34.1%; Pred. No. 6.3e-67;
Matches 240; Conservative 135; Mismatches 287; Indels 41; Gaps 10;

QY 5 SKVTQREHSSEHVTSVADLLALEPVDYKQ-SVLNVAGEAGCKKAVBEELDAED---- 59
D 44 SMTSEAQVSAARVAEAQA---RTSQP---KQISVLEALTASALNQPKTHEKVQMTKKES 97
QY 60 -----RPANWSKQYIIAQIGFSVGLGNWRFPYLCQKNGGGAYLPVLLIIIGIPFL 114
D 98 EVLLARPFWSKQYIIAQIGFSVGLGNWRFPYLCQKNGGGAYLPVLLIIIGIPFL 157
QY 115 FLELVAGQIRRGSGVWVHYICPRLGGIGFSGCIVCLFVGLYNYVIGWSIFEFKSFQY 174
D 158 FLEMAQGSMSRQGMGVNKKIAPWIGGVGYSFVFCILGLYNNVNSWIFVMSQSFQ 217

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QY 363 NEKCVVNAEKILGYLNTNVLNRDLIPPHVNFSLHTTKDYMEMDNVINMTVKEDQPSALGL 422
 Db 532 ERKVNIENV-----540
 QY 423 DPCLEDELKSVGKTGLAFIAFTAEAMTHPTSPFWSVFFLMLNLGLGSMIGMAGIT 482
 Db 541 -----ADGPGIAFVVPYEAIRLPLSPFNAIFLMLTLGLDTHFAIEIV 589
 QY 483 TPIIDT-----SKVPEKMTVGCCTFTLVGLLTVQVRSNGYFVTMPDDYSATLPLPLIVIL 538
 Db 590 TSISDEPKVLRTHKPVFTLGGCCFFITMGPPMTQGGIYMFQVLDVTAASVALVIAIF 649
 QY 539 ENTAVANIYGPCKPMQELTEMLGRPRYFYFMKFKVSPCLMAVLTIASITQLGVTPPAY 598
 Db 650 ELVGSIVYGLQRCEDEIMMIGFQPNFVKVCAEFTTILTFILCFSFYQW--EPMTY 707
 QY 599 SAWIKKEAERYLYFPNPMALLITLIVVATLPVPPVFLRHFHLLSDGSNTLSVSYKKA 658
 Db 708 GSY-----RY---PNWSVLGMLACSVINIPIMEVIKMY--LAPG-----744
 QY 659 RMKDISLENDTRFILSKVPSEAPSMPTHRSLYLGPGSTSPLETS 706
 Db 745 RFI-----ERLKLVCSPQDGPFP-LAQHGRERYKNMIDPLGTS 782
 RESULT 10
 S6A9_RAT
 ID S6A9_RAT STANDARD; PRT; 633 AA.
 AC P28572;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Sodium- and chloride-dependent glycine transporter 1 (Glyt1) (Glyt-1).
 GN SLC6A9.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RA MEDLINE=92265306; PubMed=1534013;
 RT "Cloning and expression of a glycine transporter reveal
 RT colocalization with NMDA receptors.";
 RL Neuron 8:927-935(1992).
 RN [3]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RC MEDLINE=93264081; PubMed=8494645;
 RA Borowsky B., Mezey E., Hoffman B.J.;
 RT "Two glycine transporter variants with distinct localization in the
 RT CNS and peripheral tissues are encoded by a common gene.";
 RL Neuron 10:851-863(1993).
 CC -!- FUNCTION: Terminates the action of glycine by its high affinity
 CC sodium-dependent reuptake into presynaptic terminals. May play a
 CC role in regulation of glycine levels in NMDA receptor-mediated
 CC neurotransmission.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1/GLYT-1A/GLYT-2 (SHOWN HERE)
 CC AND 2/GLYT-1B/GLYT-1; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: GLYT-1A IS FOUND IN THE GREY MATTER OF CNS AS
 CC WELL AS IN MACROPHAGES AND MAST CELLS IN PERIPHERAL TISSUES.
 CC GLYT-1B IS ONLY FOUND IN THE WHITE MATTER OF CNS.

CC CC
 CC -!- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
 CC FAMILY (SNF).
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; M95413; AAA41256.1; -;
 DR EMBL; M85595; AAA41257.1; -;
 DR EMBL; L13600; AAA73557.1; -;
 DR PIR; JH0673; JH0673.
 DR PIR; A46204; A46204.
 DR InterPro; IPR000175; Na/ntan_symport.
 DR Pfam; PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR ProDom; PD000448; Na/ntan_symport; 2.
 DR PROSITE; PS00610; NA_NEUROTRAN_SYMPT_1; 1.
 DR PROSITE; PS00754; NA_NEUROTRAN_SYMPT_2; 1.
 DR PROSITE; PS0267; NA_NEUROTRAN_SYMPT_3; 1.
 DR KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
 KW Symport; Amino-acid transport; Alternative splicing.
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 36 56 1 (POTENTIAL).
 FT TRANSMEM 64 83 2 (POTENTIAL).
 FT DOMAIN 127 127 3 (POTENTIAL).
 FT DOMAIN 128 214 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 215 233 4 (POTENTIAL).
 FT TRANSMEM 242 259 5 (POTENTIAL).
 FT TRANSMEM 295 312 6 (POTENTIAL).
 FT TRANSMEM 324 345 7 (POTENTIAL).
 FT TRANSMEM 378 397 8 (POTENTIAL).
 FT TRANSMEM 426 444 9 (POTENTIAL).
 FT TRANSMEM 460 480 10 (POTENTIAL).
 FT TRANSMEM 501 520 11 (POTENTIAL).
 FT TRANSMEM 539 557 12 (POTENTIAL).
 FT DOMAIN 559 633 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 164 164 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 167 167 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 177 177 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPPLIC 1 10 MVKGKAGML -> MAVAHGPVATSSPEQ (IN ISOFORM
 FT 2).
 SQ SEQUENCE 633 AA; 70570 MW; 7025B555B97E17 CRC64;
 Query Match 26.3%; Score 1004; DB 1; Length 633;
 Best Local Similarity 31.4%; Pred. No. 1.7e-58;
 Matches 224; Conservative 130; Mismatches 224; Indels 136; Gaps 16;
 QY 42 GEAGGKOKAVEEELDAED----RPANWSKLOVLAQIGFSGVLGNLRFPYLCOKNGGA 97
 Db 5 GAKGLMGAVPSEATKQDNLTRGNWGNQIEFVLSVGVAVGLGNVWRFPYLCYRNGGA 64
 QY 98 YLVFVLLIIIGIIPFLFLEAVGQIRRGSGVGHYICPRGLGGIFSSICVCLFVGLY 157
 Db 65 FMFYFIMLVFCGIPFLFEMELSFQGFASGCGLGVR-ISPMEKGVGYGMVWVSTYIGY 123
 QY 158 NVIIGWSITFYFPKFSQYPLPMSQC-----PVRNGSVA-VVE 193
 Db 124 NVVICIARYFYFSSMTHTVLPWAYCNPNWNTPDCAVLDASNTLNGSRPTLSHLFN 183
 QY 194 ACEKSSATTYFWYREALDISDSISGGLNWKMTCLLVNSIGMGAVKGIQSSKVM 253
 Db 184 YLQRTSPSEETWRYLVKLSDDIDGFEVRLPLGLGCLGVSWVVFLLIRGVKSGKV 243
 QY 254 YFSSFLFPPVVLACFLVRGLLLRGAVDGIILHMTFKLVKMLDPQVWREVATQVFFGLGF 313
 Db 244 YFTATFPIVVLTLFVRGVTLGSAFTGIMVLTTPKWDKILEAKVWDGDAASQIFSLGCAW 303
 QY 314 GGVIVFSSYNKODNCHFDGALVSNFTTSVLATLVFVVLGFKANIMKEKCVNAEK 373


```
Best Local Similarity 34.5%; Pred. No. 2.7e-57;
Matches 219; Conservative 110; Mismatches 200; Indels 105; Gaps 14;

Qy 28 EEPVDYKQSV-LNVAGEAGGKQ-KAVEEELDAEDRPAWNSKLOVIAQIGFVSGVGLNIWR 85
Db 22 EQLPARKTAELLVKERNGVOCCLAPRQDQAGPRETWGKKIDFLLSVGFVAVDLANVWR 81
Qy 86 FPYLCQKNGGGAYLVYVLLIIIGIPFLEAVGQIRRGISGVVWHYICPRIGGGIGFS 145
Db 82 FPYLCYKNGGGAFIPYTLFLIAGMPLFYMLAGYNEGAATVWK-ICPFKFGVGYA 140
Qy 146 SCIVCLFVGLYNNVLIIGNSIFPFKSFQYPLPWSEC-----PVVRNGSVAVVEA 194
Db 141 VILIALYGVFYNNVLIANSYLFSSFTLNLPWTDGCHTWNSPNCTDPKLLNGSVLNGHT 200
Qy 195 ECKSSAT--TVFWREALDISDS--ISESGGLNWKMTCLLVVWSTGGMAVGKGIOSG 250
Db 201 KYSKYKFTPAEFYERGVHLHSHSSIDHIGLPQWQLLCLLMVVIVLYSLWKGKVTSG 260
Qy 251 KVMYFSSLPYVVLVCLFVRLGLLGRVAVDGI---LHMFTPKLVKMLDPPQVWREVATQVFF 307
Db 261 KVMWITATLPYFVFLVLLVHGVTLPQASNGINAYLHI---DFYRLKEATVMDAATQIFF 317
Qy 308 GLGLFGGVIVFSSYNKODNCHFDGALYSFNFFTSVLATLVFVVLGFKANLMNEKV 367
Db 318 SLGAGFGVLIAPASYNKFDNNCYRALLTSSNCITTSFVSGFAIFSILGYMAH--EHKVN 375
Qy 368 VENAELKILGYNLTNLSRLDIPPHVNFSLTTKDYMEMDNVIMTKBEDQFSALGLDPCLL 427
Db 376 IE----- 377
Qy 428 EDELKSVQGTGLAFIAFTAMTHPTSPFWSVMFFLMLINLGLSGMIGMAGTTPIID 487
Db 378 ---DVATEAGLVFLYPEAISTLSGSTFWAVVFFVLLALGLDLSMGMGEAVITGLAD 433
Qy 488 TSKVPK---EMFTVCCVFTLVGLLVFVQSGNYFVTMPDDYSATLPLTLIVILENTAVA 544
Db 434 DFQVLKRLKLTFTGVTSTFLALFCITKGGIYVITLDTFAAGTSILFAVLMALGVS 493
Qy 545 WIYQPKFQMELEMTGLRPFYFYMKFVSPCLMAVLTASIIQIGVTPPAYSAWIKI 604
Db 494 WFYGVDRSNDIQMGPRPGYWRCLWKFVSPAFLLFVVVWSIINF--KPLTVDDYI-- 549
Qy 605 EAAERYLYFPNWP--MALLITLIVATLPIPVVF 636
Db 550 -----PPPWANVWGMGIALSSMVLVPYIYIY 575

RESULT 13
S6A9_BOVIN STANDARD: PRT: 638 AA.
AC Q28039; Q28040; Q29420;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium- and chloride-dependent glycine transporter 1 (GlyT1) (GlyT-1).
GN SLC6A9.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RA Jones E.M.C.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Terminates the action of glycine by its high affinity
CC sodium-dependent reuptake into presynaptic terminals. May play a
CC role in regulation of glycine levels in NMDA receptor-mediated
CC neurotransmission (by similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 3 isoforms: 1/GLYT-1B (shown here),
CC 2/GLYT-1A and 3/GLYT-1F; are produced by alternative splicing.
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CC -!- SIMILARITY: BELONGS TO THE SODIUM-NEUROTRANSMITTER SYMPORTER
CC FAMILY (SNP).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U52687; AAB01158.1; -
DR EMBL; U52688; AAB01159.1; -
DR EMBL; U52689; AAB01160.1; -
DR EMBL; U52690; AAB01161.1; -
DR InterPro; IPR000175; Na/ntran_symport.
DR Pfam; PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSMPORT.
DR ProDom; PD000448; Na/ntran_symport; 2.
DR PROSITE; PS000610; NA-NEUROTRAN_SYMPT_1; 1.
DR PROSITE; PS00754; NA-NEUROTRAN_SYMPT_2; 1.
DR PROSITE; PS00767; NA-NEUROTRAN_SYMPT_3; 1.
KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
KW Symport; Amino-acid transport; Alternative splicing.
FT DOMAIN 1 40 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 41 61 1 (POTENTIAL).
FT TRANSMEM 69 88 2 (POTENTIAL).
FT TRANSMEM 112 132 3 (POTENTIAL).
FT DOMAIN 133 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 238 4 (POTENTIAL).
FT TRANSMEM 247 264 5 (POTENTIAL).
FT TRANSMEM 300 317 6 (POTENTIAL).
FT TRANSMEM 329 350 7 (POTENTIAL).
FT TRANSMEM 383 402 8 (POTENTIAL).
FT TRANSMEM 431 449 9 (POTENTIAL).
FT TRANSMEM 465 485 10 (POTENTIAL).
FT TRANSMEM 506 525 11 (POTENTIAL).
FT TRANSMEM 544 562 12 (POTENTIAL).
FT DOMAIN 564 638 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 182 182 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPIC 1 14 MAAAQGPVASSLE -> MVKGGAKGM (IN ISOFORM
FT VARSPIC 537 638 YPSWVRVIGFLMALSSVICIPLYALFOFCDTDLHLRLK
FT NATKPSWDSGSPALLEHRTTRVAPTTPSPEDGLEVQPLHPD
FT KAOTIPMVGSSSRFQDSRI -> SSQTGLPLFTQCIAPAH
FT VPQPLSGARTSPKPKWPSVRSVLRAPLCLSDSPGSAASNPL
FT (IN ISOFORM 3).
SQ SEQUENCE 638 AA; 71318 MW; 97ADBF28EC2A443 CRC64;
Query Match 25.8%; Score 985.5; DB 1; Length 638;
Best Local Similarity 31.6%; Pred. No. 2.8e-57;
Matches 217; Conservative 124; Mismatches 214; Indels 131; Gaps 15;
Qy 50 AVEEELDAED-----RPANWSKLQVIAQIGFVSGVGLNTRPYPYLCQKNGGGAYLVYVVL 105
Db 18 AVPSEATKKDKQNLKRGWNGQIEFVLTSGVAVGLNWNRPYLYCYRNGGAGFMFPYFTM 77
Qy 106 LIIIGIPFLEAVGQIRRGISGVVWHYICPRLLGIGFSSCIYCLFVGLYNNVLIIGWSI 165
Db 78 LIIFCGIPLFFMELSFQGFASQGLGVWR-ISPMPKGVGVMWVSTYIGIYNNVVICIAF 136
Qy 166 FYFFKSFQYPLPWSEC-----PVVRNGS-----VAVVEAECEKSSA 201
Db 137 YVFFSSMTVPLWTCNNPNTPCMSVLDNPNITNGSQPPALPGVNSQALNQTAKTSP 196
Qy 202 TYFTWYREALDISDSISESGGLNWKMTCLLVVWSTGGMAVGKGIOSGKVMYFSSLPY 261
Db 197 SEBYRWRLYVLKLSDDIGNFGEVRLPGLGCLGVSWVWVFLCLIRGVKSSGVVYFTATFPY 256
Qy 262 VVLACFLVRLCLLRLGAVDGLIHMTPTKLVKMLDPPQVWREVATQVFFGLGLGGGVIVFSS 321
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Db 257 VLTLFIRGVTLEGAFGIMWYLTPOWDKILEAKVWGDAASQIFYSIGCAWGLVTWAS 316
QY 322 YNKODNCHPDGALVSPINFTSVLTLVVFVVLGFKANINNEKCVENAEKILGYLNTN 381
Db 317 YNKFHNCRDSDVLIISITNCATSVYAGVIFSLGFMAN----- 355
QY 382 VLSRDLIPPHVNFSLHTTKDYMENDNVIMTVKEDQFSALGDLPCLLLELDKSVQGTGLA 441
Db 356 -----HLGVDVSRVAD-----HGPGIA 372
QY 442 FIAFTAMTHPTSPFWSVMFMLNLGLGSMIGTMAGITPTIIDTSKVPKEMF----- 496
Db 373 FVAYPEALTLPISPLMSLFFMLLLGLGCTQCLLETITVAIVD--EVGNEWILQKKT 430
QY 497 --TVGCCVFTFLVGLLVSORSGNVFTMEDDYSATLPLTLVILENTAVAWIYQPKRFMQ 554
Db 431 VYVLGVAVAGFLGICPLTSGAGIYWLMDNYAASFSLVISCIMCVSIMIYGHQNVFQ 490
QY 555 ELTEMLGFRPYRFYFYMFKVSPCLMAVLJTASIIQLGVTTPPAYSAWIKKEAERYLYFP 614
Db 491 DIOMLGLFPPLPFQICWREVSPIAIFLIFSVIQ--YQPTVYNY-----QYP 538
QY 615 NRPMAL--LITLIVATLPTVVVFLRHFLHLLSDGNTLSVSYKKARMKDIS--NLEND 671
Db 539 SWVRIGFUMALSSVICPIYALFQF----CRTDGDGTLHRLKNATKPSRDWGPALLEHR 594
QY 672 EYRFILSKVPSEAPSP-----MPTH 691
Db 595 TRRY-----APTTPSPEDGLEVOPLH 616

RESULT 14
S6A3.RAT
AC S6A3.RAT STANDARD; PRT; 619 AA.
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sodium-dependent dopamine transporter (DA transporter) (DAT).
GN SLC6A3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92054540; PubMed=1948035;
RA Kilty J.E., Lorang D., Anara S.G.;
RT "Cloning and expression of a cocaine-sensitive rat dopamine
RT transporter."
RL Science 254:578-579(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92054539; PubMed=1948034;
RA Shimada S., Kitayama S., Lin C.-L., Patel A., Nanthakumar E.,
RA Gregor P., Kumar M., Uhl G.;
RT "Cloning and expression of a cocaine-sensitive dopamine transporter
RT complementary DNA."
RL Science 254:576-578(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92111727; PubMed=1765147;
RA Giros B., el Mestikawy S., Bertrand L., Caron M.G.;
RT "Cloning and functional characterization of a cocaine-sensitive
RT dopamine transporter."
RL FEBS Lett. 295:149-154(1991).
RN [4]
RP MUTAGENESIS.
RX MEDLINE=92366546; PubMed=1502198;
RA Kitayama S., Shimada S., Xu H., Markham L., Donovan D.M., Uhl G.;
RT "Dopamine transporter site-directed mutations differentially alter
RT substrate transport and cocaine binding."

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Proc. Natl. Acad. Sci. U.S.A. 89:7782-7785(1992).
-!- FUNCTION: TERMINATES THE ACTION OF DOPAMINE BY ITS HIGH
-!- AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
-!- STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
-!- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
-!- FAMILY (SNF).
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EMBL; M80233; AAA41100.1; -
EMBL; M80570; AAA73143.1; -
EMBL; S76145; AAB21099.1; -
PIR; S20346; S20346.
InterPro; IPR000175; Na/ntran_symport.
Pfam; PF00209; SNF; 1.
PRINTS; P000176; NANEUSMPORT.
ProDom; PD000448; Na/ntran_symport; 1.
PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; 1.
PROSITE; PS00754; NA_NEUROTRAN_SYMP_2; 1.
PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.
KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
Symport.
FT DOMAIN 1 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 1 (POTENTIAL).
FT TRANSMEM 96 116 2 (POTENTIAL).
FT TRANSMEM 140 160 3 (POTENTIAL).
FT DOMAIN 161 236 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 237 255 4 (POTENTIAL).
FT TRANSMEM 264 281 5 (POTENTIAL).
FT TRANSMEM 317 334 6 (POTENTIAL).
FT TRANSMEM 346 367 7 (POTENTIAL).
FT TRANSMEM 400 419 8 (POTENTIAL).
FT TRANSMEM 446 464 9 (POTENTIAL).
FT TRANSMEM 480 500 10 (POTENTIAL).
FT TRANSMEM 521 540 11 (POTENTIAL).
FT TRANSMEM 559 577 12 (POTENTIAL).
FT DOMAIN 578 619 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 597 597 E -> K (IN REF. 3).
SQ SEQUENCE 619 AA; 68746 MW; DF3A30C981095D24 CRC64;
Query Match 25.7%; Score 981.5; DB 1; Length 619;
Best Local Similarity 35.6%; Pred. No. 4.9e-57;
Matches 213; Conservative 100; Mismatches 186; Indels 99; Gaps 11;
QY 55 LDAEDRPANWSKLOYTLAIGFSGVGLNWRPPLCYCKGKGGAVLPVLLIITGLPLF 114
Db 55 VEAQERETWSKIDFLLSVIGFAVDUANVWRPPLCYCKGKGGAVLPVLLIITGLPLF 114
QY 115 FLEAVGQIRRGSGVGHVYICPRLGIGISFCVCLFVGLYNNVIIGWSIFYPFKSFQY 174
Db 115 YMELALGOFNREGAAGVWK-ICPVLGKGVFTVLIISFYVGFVFNVIIAWALHFFSFTM 173
QY 175 PLPWESECPVVRNGSVAVVAEAEKSS-----ATTVFYREALDIDS--ISE 219
Db 174 DLPWIHCNNTWN-SPNCSDAHASNSDGLGLNDFTGTTAAAEYF-ERGVLRHLHQSGIDD 231
QY 220 SGGLNWKMTLCLLVWVSIGGMVAGKGIQSSKVMYFSSLPYVVLACFLVRGLLLCAVD 279
Db 232 LGPPRQULATCLVLLVLLYFLSLWKGVKTSKGVWITATMPYVVLATLLRGTLPFCAMD 291
QY 280 GILHMFTEPKLMKLDPOVMREVATQVFFGLGLGFGVGVIVFSSYNKQDNCHDFGALVSFI 339

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Db 292 GIRALVSDVDFYRLCRASVWDAATQVCSIGVGVGLIAFSSYNKFNCCYRDALITSI 351
 QY 340 NFFTSVLATLVVGVGLFANIMNEKCVVENAEKILGYLNTNVLSDRLIPPHVNFSLHT 399
 Db 352 NSLTSFGVGVVFSFLGMAQ-----KHNVPIDV----- 381
 QY 400 KDMEMDNVIMTKEDQFSALGLDPCLEDELKDSVQGTGLAFIAFTAEAMTHFTPTSPWS 459
 Db 382 -----ATDGPLIIFIYPEATATPLSSAWA 407
 QY 460 VMFFLLMLNLGLSGMIGTMAGITTPIDTSKV---PKEMFTVGCCTFLLVGLLFVORSG 516
 Db 408 AVFFLLMLLTGLDSAMGMSVITGLVDFOLHRRHRELFTGLVLAFLLSLFCVTNGG 467
 QY 517 NYFVTMDDYSATLPLTLVILENAVANIYGPKEQWELTEMLGFRPFRFYFYMMKFSVS 576
 Db 468 IYVFTLLDHFHAAGTSILFGVLEAIGAFAVFGVQOQSDDIKQMTGQRPNLYWRCLKLVLS 527
 QY 577 PLCMAVLTTASIIQLGVTPPAYSAWIKKEAERYLYFPNPMAL--LITLIVVATLPI 632
 Db 528 PCFLLYVVVSVITP--RPHYGAYI-----FPDNALGLWIIATSSMAWVPI 573

RESULT 15

S6A9_MOUSE STANDARD; PRT; 633 AA.
 AC P2857L1;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Sodium- and chloride-dependent glycine transporter 1 (Glyt1) (Glyt-1).
 GN SLC6A9 OR Glyt1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 .RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92316254; PubMed=1618338;
 RA Liu Q.-R., Nelson H., Mandiyan S., Lopez-Corcueru B., Nelson N.;
 RT "Cloning and expression of a glycine transporter from mouse brain."
 FEBS Lett. 305:110-114(1992).
 CC -!- FUNCTION: Terminates the action of glycine by its high affinity
 sodium-dependent reuptake into presynaptic terminals. May play a
 role in regulation of glycine levels in NMDA receptor-mediated
 neurotransmission.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; GLYT-1A (SHOWN HERE) AND GLYT-
 1B; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
 FAMILY (SNF).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X67056; CAA47440.1; -;
 DR PIR; S23151; S23151.
 DR MGD; MGI:95760; Glyt1.
 DR InterPro; IPR000175; Na/ntran_symport.
 DR Pfam; PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR ProDom; PD000448; Na/ntran_symport; 2.
 DR PROSITE; PS00610; NA_NEUROTRAN_SYMPT_1; 1.
 DR PROSITE; PS00754; NA_NEUROTRAN_SYMPT_2; 1.
 DR PROSITE; PS0267; NA_NEUROTRAN_SYMPT_3; 1.
 DR Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
 KW

Symport; Amino-acid transport; Alternative splicing.
 DOMAIN 1 35
 TRANSMEM 36 56
 TRANSMEM 64 83
 TRANSMEM 107 127
 DOMAIN 128 214
 TRANSMEM 215 233
 TRANSMEM 242 259
 TRANSMEM 295 312
 TRANSMEM 324 345
 TRANSMEM 378 397
 TRANSMEM 426 444
 TRANSMEM 460 480
 TRANSMEM 501 520
 TRANSMEM 539 557
 DOMAIN 559 633
 CARBOHYD 164 164
 CARBOHYD 167 167
 CARBOHYD 177 177
 CARBOHYD 183 183
 VARSPLIC 1 10
 SEQUENCE 633 AA; 70775 MW; PD64AA561F470793 CRC64;
 Query Match 25.7%; Score 981.5; DB 1; Length 633;
 Best Local Similarity 31.3%; Pred. No. 5e-57;
 Matches 217; Conservative 126; Mismatches 220; Indels 131; Gaps 15;
 QY 42 GEAGGKQKAVEEELDAED---RPAWNSKLOYILAOIGFVGLGNWRPILYCKQNGGGA 97
 Db 5 GAKGMLGAVPSEATKDDQNLTGRNWNQIEFVLTSGVAVGLGNWRPILYCYRNGGGA 64
 QY 98 YALPYLVLLIIIGIPFLELAVGQIRRGISGVVHYICPRLGIGFSSICVLCFLVGLYY 157
 Db 65 FMPEYFIMLIFCGIPLEFMELSFQFASQCGLGVR-ISPMEKGVGYGMVSTYIGIYY 123
 QY 158 NVLIIGSIFFFKSFQYPLPWSK-----PVRNGSVA-VVE 193
 Db 124 NVVICIAFYFFSSMTHVLPWAYCNPNWTPDCAGVLDASTNRSRPAALSNLSHLFN 183
 QY 194 AECEKSSATFYFYREALDISDSISESGLNWKMNTLCLLVVWSIGGMAYGKIQSSGKVM 253
 Db 184 YTLQTSFSEYWRLYLVKLSDDIGNFCEVRLPLGLGSGVWVWVFLCLIRGVKSGKV 243
 QY 254 YFSLFFVYVVLACFLVRLGLLRGAVDGIHMETPKLVKMLDPOVWREVATQVFFGLGLGF 313
 Db 244 YFTATFPPVVLITLVFVGVTELEAGFTIMYLTLPQMDKYLEAKVWGDAAASQIFYSGLCAW 303
 QY 314 GGIVFSSYNKQDNNDNCHDFDGLVSPINFTSVLATLVFVFLGFKANIMNEKCVVENAEK 373
 Db 304 GGLITMASYNKFNHNCYRDSVLIISITNCATRLYAGFVIFSLGFMAN----- 350
 QY 374 ILGYLNTNVLSDRLIPPHVNFSLHTTKDYMENDNIMTVKEDQFSALGLDPCLEDELK 433
 Db 351 -----HLGVDVSRVAD----- 361
 QY 434 SVQGTGLAFTAEAMTHFTPTSPFWSVFMFLMLNLGLSGMIGTMAGITPIIDTSKVPK 493
 Db 362 --HGPGLAFVAYPEALTLPLSPLSLFFMLILGLGTQCLLETFLVTAIVD--EVGN 417
 QY 494 EMF-----TVGCCVFTFLVGLLFVQSRSGNVFTVMDFDYSATLPLTLVILENAVANI 546
 Db 418 EWILQKQTYVTGLGAVAGFLIGIPLTQSAGIYVLLMDNYAASFSLVLSICMVSIMYI 477
 QY 547 YGPKFMQELTEMLGFRPFRFYFYMMKFSVPLCMVLTASIIQLGVTPPAYSAWIKKEA 606
 Db 478 YGHRNYEQDIQMMLGFPPLFPFQICWRFSVPAIIFFLIFTVIQ--YRPITYN----- 528
 QY 607 AERYLYPNWPMAL--LITLIVVATLPPVVFVLRHFLHLLSDGSNTLSVSYKKRMMKDI 664
 Db 529 ---HYQYPGMAVRIGFLMALSSVICIPLVALFOL-----CRTDGDTLQLRUKNATKPSRDW 581
 QY 665 S-NLEENDETRFILLSKVPSEASP-----MPTH 691

Mon Apr 21 19:59:15 2003

us-09-923-444a-2.rsp

Page 15

Db 582 GPALLEHRTGRY----APTTTPSPEDGFEVQPLH 611

Search completed: April 21, 2003, 13:56:00
Job time : 30 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 13:53:57 ; Search time 48 Seconds
(without alignments)
1456.036 Million cell updates/sec

Title: US-09-923-444A-2

Perfect score: 3817

Sequence: 1 MPKNSKVQREHSSSEHVTES.....NPNPGYRGYLLASTPESEL 727

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3610	94.6	727	2 S27043	neurotransmitter t
2	3595	94.2	727	2 I56506	Na+/Cl(-)-dependen
3	2483	65.1	730	2 I52632	sodium-dependent n
4	2463	64.5	728	2 I65413	sodium-dependent n
5	1302.5	34.1	616	2 S09998	transporter protei
6	1028	26.9	799	2 A48716	glycine transporte
7	1004	26.3	633	2 I58140	glycine transporte
8	1003	26.3	638	2 JH0673	glycine transporte
9	997.5	26.1	638	2 I77912	glycine transporte
10	995.5	26.1	692	2 I57956	glycine transporte
11	985.5	25.8	617	2 S14278	noradrenaline tran
12	981.5	25.7	619	2 S20346	dopamine transport
13	981.5	25.7	619	2 I59558	dopamine transport
14	981.5	25.7	633	2 S23151	glycine transporte
15	975.5	25.6	635	2 A46061	Na(+)-dependent cr
16	974.5	25.5	635	2 S23431	choline transport
17	973.5	25.5	635	2 JC2386	creatine transport
18	968.5	25.4	614	2 A41757	betaine transport
19	966.5	25.3	599	1 ACRTGT	gamma-aminobutyric
20	965.5	25.3	620	2 A48980	dopamine transport
21	965	25.3	620	2 I57937	dopamine transport
22	963.5	25.2	637	2 JH0674	L-proline transport
23	963	25.2	635	2 G02095	creatine transport
24	962.5	25.2	615	2 S43285	noradrenaline tran
25	957.5	25.1	602	2 I55651	noradrenaline tran
26	955.5	25.0	620	2 S46487	taurine transporte
27	955	25.0	614	2 S68236	betaine/GABA trans
28	953	25.0	611	2 S46260	creatine transport
29	951.5	24.9	599	2 S11073	gamma-aminobutyric

30 951.5 24.9 620 2 G01426 taurine transporte
31 951 24.9 602 2 A44409 gamma-aminobutyric
32 951 24.9 602 2 A45078 gamma-aminobutyric
33 948.5 24.8 614 2 A43390 gamma-aminobutyric
34 947 24.8 607 2 S19585 serotonin transport
35 943.5 24.7 630 2 S30604 neurotransmitter t
36 941.5 24.7 655 2 A46270 Na and Cl dependen
37 937.5 24.6 630 2 A47398 serotonin transport
38 937 24.5 693 2 A41617 dopamine transport
39 928.5 24.3 619 2 S29839 taurine transport
40 925.5 24.2 621 2 I57939 taurine transport
41 924 24.2 598 2 F46027 gamma-aminobutyric
42 923.5 24.2 627 2 JH0695 gamma-aminobutyric
43 917 24.0 598 2 I51368 gamma-aminobutyric
44 915.5 24.0 627 2 B44409 GABA transport pro
45 914 23.9 597 2 S65673

ALIGNMENTS

RESULT 1

S27043

neurotransmitter transport protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999

C:Accession: S27043

R:Lib: Q.R.; Mandliyan, S.; Lopez-Corcuera, B.; Nelson, H.; Nelson, N.

FEBS Lett. 315, 114-118, 1993

A:Title: A rat brain cDNA encoding the neurotransmitter transporter with an unusua

A:Reference number: S27043; MUID:93114444; PMID:8093354

A:Accession: S27043

A:Molecule type: mRNA

A:Residues: 1-727 <LIID>

A:Cross-references: GB:S22051; MID:G262842; PIDN:AAB24776.1; PID:G262843

C:Superfamily: gamma-aminobutyric acid transporter

C:Keywords: transmembrane protein

Query Match 94.6%; Score 3610; DB 2; Length 727;

Best Local Similarity 94.4%; Pred. No. 2.6e-278;

Matches 686; Conservative 13; Mismatches 28; Indels 0; Gaps 0;

Qy	1	MPKNSKVQREHSSSEHVTESVADLLALEPVDYKQSVNLNVAAGGKQKAVEBELDAEDR	60
Db	1	MPKNSKVQREHSSSEHVTESVADLLALEPVDYKQSVNLNVAAGTGGKQKVAEBELDAEDR	60
Qy	61	PAWNSKLOYLIAQIGFSGVLGNWRPPYLCQKNGGAYLVPYLVLLIIIGIPLFFLEAV	120
Db	61	PAWNSKLOYLIAQIGFSGVLGNWRPPYLCQKNGGAYLVPYLVLLIIIGIPLFFLEAV	120
Qy	121	GQIRRGSTGVWHYICPRLGIGFSSCIIVCLFVGLYNNVTIGWSIFVFFKSFQYPLPWSE	180
Db	121	GQIRRGSTGVWHYICPRLGIGFSSCIIVCLFVGLYNNVTIGWSIFVFFKSFQYPLPWSE	180
Qy	181	CPVWRANGSVAVVEAECEKSATTYFWYREALDISDSISESGGLNWKMTCLLLVWVSIGGM	240
Db	181	CPVIRNGTAVVVEPECEKSATTYFWYREALDISDSISESGGLNWKMTCLLLVWVSIGGM	240
Qy	241	AVGKGIQSSGKVMYSSLPYPVVLACFLVRLGILLRGAVDGILHMFPTKLVKMLDPQVRE	300
Db	241	AVVGIQSSGKVMYSSLPYPVVLACFLVRLGILLRGAVDGILHMFPTKLVKMLDPQVRE	300
Qy	301	VATQVFFGLGLGFGVGVVFFSSYNKQDNCHFGALVSFFNFFTSVLTATLVVFFVVLGPKAN	360
Db	301	AATQVFFGLGLGFGVGVVFFSSYNKQDNCHFGALVSFFNFFTSVLTATLVVFFVVLGPKAN	360
Qy	361	IMNEKCVVENAEKILGYLNTNVLSDRLLIPPHVNFSLHLLTKDYMEMDNVIMTVKEDQFSAL	420
Db	361	IMNEKCVVENAEKILGYLNSVLSRDLIPPHVNFSLHLLTKDYSEMYNVIMTVKEDQFSAL	420
Qy	421	GLDPCLLDELDKSVQGTGLAFIAFTEAMTHFTSPFWSVMFFLMLINLGLSGNIGTMAG	480
Db	421	GLDPCLLDELDKSVQGTGLAFIAFTEAMTHFTSPFWSVMFFLMLINLGLSGNIGTMAG	480

QY	481	I T P I I D T S K V P K E M F T V G C C V F T L V G L L F V Q R S G N F V T M D D Y S A T P L P U T L V I L E N	540
Db	481	I T P I I D T E K P K E M F T V G C C V F A F P V G L F V Q R S G N F V T M D D Y S A T P L P U T L V I L E N	540
QY	541	I A V A W I Y G P K K M O E L T E M L G R P Y R F E Y M K K F V S P C M A V L T T A S I I Q L G V T P P A Y S A	600
Db	541	I A V A W I Y G K K M O E L T E M L G R P R F R F Y M K F V S P C M A V L T T A S I I Q L G V S P P G Y S A	600
QY	601	W I K E E A A R Y L F P N P M A L L I T I V A T L P I P V F V L R H R F H L L S D G S N T L S V S Y K K A R M	660
Db	601	W I K E E A A R Y L F P N W A M A L L I T I A V A T L P I P V F I L R H R F H L L S D G S N T L S V S Y K K G R M	660
QY	661	M K D I S N L E N D E T R F I L S K V P S E A S P M P T H R S Y L G P G S T S P L E T S W P N G P Y G R G Y L L A	720
Db	661	M K D I S N L E N D E T R F I L S K V P S E A S P M P T H R S Y L G P G S T S P L E S S H P N G R Y G Y L L A	720
QY	721	S T P E S E L 727 	
Db	721	S T P E S E L 727 	
RESULT 2			
I56506			
Na+/Cl(-)-dependent neurotransmitter transporter, brain - rat			
C:Species: Rattus norvegicus (Norway rat)			
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Aug-1999			
C:Accession: I56506			
R;el Westikawy, S.; Giros, B.; Pohl, M.; Hamon, M.; Kingsmore, S.F.; Seidlin			
J. Neurochem. 62, 445-455, 1994			
A:title: Characterization of an atypical member of the Na+/Cl(-)-dependent			
A:Reference number: I56506; MUID:94125086; PMID:8294906			
A:Accession: I56506			
A>Status: preliminary; translated from GB/EMBL/DBDJ			
A:Molecule type: mRNA			
A:Residues: 1-727 <RES>			
A:Cross-references: GB:I568944; NID:g545077; PIDN:AAC60673.1; PID:g545078			
C:Superfamily: gamma-aminobutyric acid transporter			
Query Match 94.2%; Score 3595; DB 2; Length 727; Best Local Similarity 94.1%; Pred. No. 4-le-277; Matches 684; Conservative 13; Mismatches 30; Indels 0; Gaps			
QY	1	M P N K S K V T Q R E H S S E H V T S V A D L L A L E P P V D Y K Q S V L N V A G E A G K Q K A V E E L D A E D R	60
Db	1	M P N K S K V T Q R E H S S E H V T S V A D L L A L E P P V D Y K Q S V L N V A G E T G K Q K A V E E L D A E D R	60
QY	61	P A N N S K L Q Y L T A I G F S V G L N T W R P P Y L C Q K N G G A Y L P V L V L L I I T I G I P L F F L E L A V	120
Db	61	P A N N S K L Q Y L T A I G F S V G L N T W R P P Y L C Q K N G G A Y L P V L V L L I I T I G I P L F F L E L A V	120
QY	121	G Q R I R R G S I G W H Y I C P R L G G I G F S S C I V C L F V G L Y N V I I G W S I P Y F P K F S Q Y P L P W S E	180
Db	121	G Q R I R R G S I G W H Y V C P R L G G I G F S S C I V C L F V G L Y N V I I G W S V F Y F P K F S Q Y P L P W S E	180
QY	181	C P V V R N G S V A V A E C E K S A T T Y F W Y R E A L D I S D S I S E S G G L N K W M T L C L L V A W S I G M	240
Db	181	C P V I R N G T A V A P E C E K S A T T Y F W R E A L D I S N S I S E S G G L N K W M T V C L L V A W S I G M	240
QY	241	A V G K I Q S S K V M Y F S S L P F Y V V Y A C L F V R G L L R G A V D P G I L H M F T P K L V K M L D P Q W R E	300
Db	241	A V K V I Q S S K V M Y F S S L P F C V V L A C L F V R G L L R G A V D P G I L H M F T P K D K M L D P Q W R E	300
QY	301	V A T Q V P F G L G L G G V G Y I V S S Y N K Q D N C H F D G A L V S F I N F T S V L A T L V F V F W L G F K A N	360
Db	301	A A T Q V F F A L G L G G V I A F S S Y N K Q D N C H F D A A L V S F I N F T S V L A T L W F A V I G L F K A N	360
QY	361	I M N E K C V V N A E K I L G Y N T N V L S R D L I P P H V N F S H L T K D Y M E M D N V I M T V K E D Q F S A L	420
Db	361	I M N E K C V V N A E K I L G Y L N S N V L S R D L I P P H V N F S H L T K D Y S E M Y N V I M T V K E Q F S A L	420
QY	421	G L D P C L L E D E L D K S V G T G L A F T A F T E A M T H F P T S P F S W S V F F L M I N I L G L S M I G T M A G	480

Db 415 KEEFAVLHLKACQIEDLNAVQCTGLAFIAFTEAMTHFPASPFWSMFELMLNLGLG 474
QY 473 SMIGTMAGITPIIDTSKVPKEMFTVGCCTFLVGLLQVQSGNFFVTMFDDYSATLPL 532
Db 475 SMFTGIIIPVVDTFKVRKEILTICCLAFICGLMEVQVSGNFFVTMFDDYSATLPL 534
QY 533 TLIVILENIAVAVTYGPKKQOELEMLGFRPYRFYFMWKFVSPCLCMVAVLTASTIOLG 592
Db 535 LIVIVILENIAVSFVGIDKFLIEDLMLGFPAPSKYIYMWKYSPLMLVTLIASIVNMG 594
QY 593 VTPPAYSAWIKKEAAERYLYFPNPMALLITLIVVATLPVPVFLRHFHLLSDGS-NPL 651
Db 595 LSPGYNAWIKKEASEEFLSYPMGMVVCESLWLVAILPVPVFIIRCNLLIDSSGNLA 654
QY 652 SVSYKKARMKDISNLEENDETRFILSKVPSEAPSPMTHRSYLGPGSTSPLETSWNPG 711
Db 655 SVTYKRGVLPKPNL-DGDDASLIHGKIPSEMSPNFGKNIYRKQSGSPTLDTA--PNG 711
QY 712 PYGRGYLLA---STPESEL 727
Db 712 RYGILMADMPDMPESDL 730

RESULT 4

I65413
sodium-dependent neurotransmitter transporter - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Aug-1999
C:Accession: I65413
R:Uhl, G.R.; Kitayama, S.; Gregor, P.; Nanthakumar, E.; Persico, A.; Shimada, S.
Brain Res. Mol. Brain Res. 16, 353-359, 1992
A:Title: Neurotransmitter transporter family cDNAs in a rat midbrain library: 'orphan' tr
A:Reference number: I52632; MUID:93180651; PMID:136329
A:Accession: I65413
A:Status: preliminary;
A:Molecule type: mRNA
A:Residues: 1-728 <RES>
A:Cross-references: GB:S56968; NID:q298323; PIDN:AAB25532.1; PID:q298324
C:Superfamily: gamma-aminobutyric acid transporter

Query Match 64.5%; Score 2463; DB 2; Length 728;
Best Local Similarity 63.6%; Pred. No. 2.8e-187;
Matches 469; Conservative 109; Mismatches 135; Indels 24; Gaps 8;

QY 4 NSKVQREHSSHEVTESVADLLALEPVD--YKQSVLVNAGPAGKQKXAVEELDAED-- 59
Db 3 NSKVVRKD-LDDVIESVKDLLSNEDESVKSKSELIVDQE-----EKDQAEDEGS 54
QY 60 ----RPAWNSKQYILAQIGFSVGLGNIRFPYLCQKNGGAYLPVYLVLIIIGIPLF 114
Db 55 EVDDERPAWNSKQYILAQIGFSVGLGNIRFPYLCQKNGGAYLPVYLVLIIIGIPLF 114
QY 115 FLELVAGQRRRIGISGVVHYICPLRGIGTGFSSCIVCLFVGLYVNYIOWSIPIYFKSPQY 174
Db 115 FLELVAGQRRRIGISGVVHYISPLRGIGTGFASCVVYXVYALYNIIGWTLFYFSQSFQ 174
QY 175 PLPWSECPVVRNGSVAVVAAECESKSSATTYEYREALDISDSISPSGGLNWKMTLCILVV 234
Db 175 PLPWQDQPLVKNASHTYIECEKSSATTYEYREALDISDSISPSGGLNWKMTLCILAX 234
QY 235 WSTIGAVGKIQSGKGVYESSLPFYVYLACFLVRGLLGRGAVDGIILHMFPPKLVKMLD 294
Db 235 WVVVCLAMIRGIQSGKIMYESSLPFYVYLICFLIRSLLLNGSIDIRHMFPPKLEMLLE 294
QY 295 PQVWREVATQVFGGLGFGGVIVFSSYNKQDNCHFDGALVSFINFTSVLATLVFVYV 354
Db 295 PKVWREATAQVFFALGLGFGGVIAFSSYNKRDNNCHFDVAVLSFINFTSVLATLVFVAV 354
QY 355 LGFKANIMNEKCVVNAEKILGYLNTNVLNRDLIPPHNFSLHITTKDYEMDNVIMTKVE 414
Db 355 LGFKANIVNEKCIQNSSEMILKLLXTGNVSWDVIPRHINLSAVTAEDYHVVYDIIOKVE 414

QY 415 DQFSALGLDCLLEDELDSVQGTGLAFIAFTEAMTHFTPTSPFWSMFELMLNLGLGSM 474
Db 415 BEFAVLHLKACQIEDLNAVQCTGLAFIAFTEAMTHFPASPFWSMFELMLNLGLGSM 474
QY 475 IGTMGITPIIDTSKVPKEMFTVGCCTFLVGLLQVQSGNFFVTMFDDYSATLPL 534
Db 475 FGTGEGITPIVDTFKVRKEILTICCLAFICGLMEVQVSGNFFVTMFDDYSATLPL 534
QY 535 IVILENIAVAVTYGPKKQOELEMLGFRPYRFYFMWKFVSPCLCMVAVLTASTIOLGVT 594
Db 535 WILENIAVSFVGIDKFLIEDLMLGFPAPSKYIYMWKYSPLMLVTLIASIVNMGUS 594
QY 595 PPAYSAWIKKEAAERYLYFPNPMALLITLIVVATLPVPVFLRHFHLLSDGS-NPL 653
Db 595 LSPGYNAWIKKEASEEFLSYPMGMVVCESLWLVAILPVPVFIIRCNLLIDSSGNLASV 654
QY 654 SYKKARMKDISNLEENDETRFILSKVPSEAPSPMTHRSYLGPGSTSPLETSWNPGY 713
Db 655 TYKRGVLPKPNL-DGDDASLIHGKIPSEMSPNFGKNIYRKQSGSPTLDTA--PNGRY 711
QY 714 GRGYLLA---STPESEL 727
Db 712 GIGYLMADMPDMPESDL 728

RESULT 5

S50998
transporter protein (clone rB21a) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C:Accession: S50998
R:Smith, K.E.; Fried, S.G.; Durkin, M.M.; Gustafson, E.L.; Borden, L.A.; Branchek, F.E.S. Lett. 357, 86-92, 1995
A:Title: Molecular cloning of an orphan transporter. A new member of the neurotrans
A:Reference number: S50998; MUID:95094940; PMID:8001687
A:Accession: S50998
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-616 <SMI>
A:Cross-references: GB:S76742; NID:g914027; PIDN:AAB32806.1; PID:g914028
C:Superfamily: gamma-aminobutyric acid transporter

Query Match 34.1%; Score 1302.5; DB 2; Length 616;
Best Local Similarity 43.1%; Pred. No. 2.9e-95;
Matches 265; Conservative 122; Mismatches 191; Indels 37; Gaps 14;

QY 38 LNVAGEAGGKQKAVEEELDAED----RPAWNSKQYILAQIGFSVGLGNIRFPYLCQKN 93
Db 3 LAIKRRASRGQRFQDEKRADEMEKARPQWGNPLQFVFACISYAVGLGNVWRFPYLCQMY 62
QY 94 GGGAYLPVYLVLIIIGIPLFLELVAGQRRRIGISGVVHYICPLRGIGTGFSSCIVCLFV 153
Db 63 GGSFLVPYLIIMLIVEGMPLLYLELVAGQRRRIGISGVVHYICPLRGIGTGFSSCIVCLFV 122
QY 154 GLYNYVNIIGHSIFYFESQYPLPWSQCPVVRNGSVAVVAAECESKSSATTYEYREALDI 213
Db 123 SMYVNVINAGFWYLFHSDPDPWVCPL--NSNRTGYDECEKASSTQYFMYRKTUNI 180
QY 214 SDSISESGGLNWKMTLCILVWSTGGMAVGKIOSSGKVMYFSSLPFYVYLACFLVRGLL 273
Db 181 SPISQENGQVQWEPALCLTLAWLMVYLCLRGTESTGKVVYFTALMPYCVLIYILVRGLT 240
QY 274 LRGAVDGILHMFPPKLVKMLDPOVWREVATQVFGGLGFGGVIVFSSYNKQDNCHFDG 333
Db 241 LRGATNGLMYTFPKIEQLANPKAWINAAQTIFSLGSLGSLIAFASYNPSNDCQKHA 300
QY 334 ALVSNFNTSVLATLVVFWVVLGFKANIMNEKCVVNAEKILGYLNTNVLNRDLIPPHNV 393
Db 301 VIIVSVINSSTSIASIVTSFYGKATFNENCL----NKVI-LLLTN--SFDL-----E 348
QY 394 FSLHTTKDYEMDNVIMTKVEDQFSAL--GLDPCLEDELDSVQGTGLAFIAFTEAMTH 451
Db 349 DGLFELASNLEEVKDYLASTVYPNKYSEVFPPIRNCSELNLTAVQGTGLAFIVAEAIKN 408

[illegible]

Db 352 NSLTSFSSGFWFSLGYMAQ-----KHNVPIRDV----- 381

352 NSITPSSCEWVESEI CYMAO-----KUNWOTDOW 307

352 NSITPSSCEWVESEI CYMAO-----KUNWOTDOW 307

QY 400 KDMEMDNVIMTKEDQFSAIGLDPCLLEDELDKSVQGTGLAFIAFTAMTHEFTSPFWS 459
Db 382 -----ATDGPGLIFIYPEAIATLPLSSAWA 407
QY 460 VNFELMLINLGLSGMTGWTAGITPIIDTSKV---PKEMFTVGCCTFFLVGLLFFVQRSG 516
Db 408 AVFFELMLLGLDSAMGSMGVITGLVDFQFLLHRRHELETLGLVATFELLSFCVTCNGG 467
QY 517 NYFVTFMEDDYSATLPLTLVLILENIAVANIYGPCKFMQELTEMLGFRPYRYFYFWMKREVS 576
Db 468 IYVFTLLDHFAGAGTSILFGLVLEAIGAVNYFYQQQFDDIKQMTGQRPNLYWRCLWKLUVS 527
QY 577 PLCAVLTATASIQLQVTPPAYSAWIKKEAAERYLYFPNPNMAL--LITLIVATLPI 632
Db 528 PCFLILYVVVSVITF--RPHYGYI-----PPDNALGLWIIATSSMAWPI 573
RESULT 14
S23151
glycine transporter protein GLYTla - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C:Accession: S23151; B48716
R:Li, Q.R.; Nelson, H.; Mandiyan, S.; Lopez-Corcuera, B.; Nelson, N.
FEBS Lett. 305, 110-114, 1992
A:Title: Cloning and expression of a glycine transporter from mouse brain.
A:Reference number: S23151; MUID:92316254; PMID:1618338
A:Accession: S23151
A:Molecule type: mRNA
A:Residues: 1-633 <LIU>
A:Cross-references: EMBL:X67056; NID:g51092; PIDN:CAA47440.1; PID:g51093
R:Li, Q.R.; Lopez-Corcuera, B.; Mandiyan, S.; Nelson, H.; Nelson, N.
J. Biol. Chem. 268, 22802-22808, 1993
A:Title: Cloning and expression of a spinal cord- and brain-specific glycine transporter
A:Reference number: A48716; MUID:94043045; PMID:8226750
A:Accession: B48716
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <LI2>
C:Genetics:
A:Gene: GLYT1
C:Superfamily: gamma-aminobutyric acid transporter
C:Keywords: alternative splicing; transmembrane protein
Query Match 25.7%; Score 981.5; DB 2; Length 633;
Best Local Similarity 31.3%; Pred. No. 9e-69;
Matches 217; Conservative 126; Mismatches 220; Indels 131; Gaps 15;
QY 42 GRAGGKQKAVEBELDAD-----RPAWNSKLOYILAOIGFSGVLGNIRFPYLCQKNGGGA 97
Db 5 GARGMLNGAVPSBATKKDQNLTRGNMGNQIEFVLTSVGYAVGLGNVWRFPYLCYRNGGGA 64
QY 98 YLVPYLVLLIIIGIPFLFELAVQGTIRRGISGVWHYICPLRGIGFSSCIVCLFVGLY 157
Db 65 FNEPFIIMLFCGIPFLFELFELSGFQFASQCLGVWR--ISPMEKGVGYGMVVSTVIGIY 123
QY 158 NVIIGNSIFYFFKSFQYPLPWSSEC-----PVRNSVA--VVE 193
Db 124 NVVICIAFYFFSSMTHVLPWAYCNPWNTPDCAVLDASNLNTRSRPAALSGNLSHLFN 183
QY 194 ABECKSSATYFMYREALDSDTSSESGLNWKMTCLLVVWS:TCGMAVGKIOSGKVM 253
Db 184 YTLQRTSPSEYWRLLVYKLUSDGIDNIGFGEVRLPLGLCLGDSVWVVFCLIRGSGKVV 243
QY 254 YFSSLPYVVLVACFLVRLGAVDGIILHMFTEPKLKMPLDQVWREVATQVFFGLGLGF 313
Db 244 YFTATPYVVLTLFVRGVTLEGFTGIMYLTQWDKYLEAKYWGDAASQIFYSLGCAW 303
QY 314 GGIVFSSYNKONNCHFDGALVSFINFTSVLATLVVVFVGLGFKANIMNEKCVVNAEK 373
Db 304 GGLITMASYNKFNHCYRDSVITSITNCATRLYAGVIFSLGFMAN----- 350
QY 374 ILGLYLTNTVLSRLDILPHVNFSLHTTKDYMEDMNDVIMTKEDQFSAIGLDPCLLEDELDK 433

Db 351 -----HLGVDVSRVAD----- 361
QY 434 SVQGTGLAFTAFTEAMTHEFTSPFWSVWFLLMLINLGLSGMTGWTAGITPIIDTSKVPK 493
Db 362 --HCPGLAFAYPEALTLPLISPLWSLFFLFFMLILGLGTCQCLLETULTAIVD--EVGN 417
QY 494 EMF-----TVGCCVFTFLVGLLFFVORSNGVFTVMFDYDYSATLPLTLVLILENIAVAWI 546
Db 418 EWILQKTYTTLGVAVAGVLLGIPLTSAAGIYWLMLMDNYAASFSVLVISCIMCVSIMYI 477
QY 547 YGPKFKMQELTEMLGFRPYRYFYFWMKREVSPLCMAVLTATASIQLQVTPPAYSAWIKKEA 606
Db 478 YGHRNVFQDIOMLGMFPPLFFQICWREVSPLAIFELIFTVIQ--YRDTYN----- 528
QY 607 AERYLYFPNPNMAL--LITLIVATLPIPVVFLRHFHLLSDGNTLSVSYKKARMMKDI 664
Db 529 ---HYQYPGWAVRIGFLMALSSVICIPLYALFQL-----CRTDGDTLQLRLKNATKPSRDW 581
QY 665 S-NLEENDETRFILSKVPSEAPSP-----MPTH 691
Db 582 GPALLEHRTGRY----APTTPSPEDGFEVQPLH 611
RESULT 15
A46061
Na(+)-dependent creatine transporter - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
C:Accession: A46061
R:Guimbal, C.; Killmann, M.W.
J. Biol. Chem. 268, 8418-8421, 1993
A:Title: A Na(+)-dependent creatine transporter in rabbit brain, muscle, heart, and
A:Reference number: A46061; MUID:93231984; PMID:8473283
A:Accession: A46061
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-635 <GUI>
A:Experimental source: brain and muscle
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:129571, NCBI:129580)
C:Superfamily: gamma-aminobutyric acid transporter

Query Match 25.6%; Score 975.5; DB 2; Length 635;
Best Local Similarity 33.4%; Pred. No. 2.7e-69;
Matches 204; Conservative 108; Mismatches 188; Indels 111; Gaps 14;
QY 60 RPAWNSKLOYILAOIGFSGVLGNIRFPYLCQKNGGAYLVPLVLLIIIGIPFLFLELA 119
Db 52 RETWTRQMDFTMSCVGAVGLGNVWRFPYLCYKNGGVELIIPYLVLLVGVGIFFELEIS 111
QY 120 VGORIRRGISGVWHYICPLRGIGFSSCIVCLFVGLYINVIIGWSIFYPFKSFQYPLPWS 179
Db 112 LGQFMKAGSINVN--ICPLFKGLGVASVMVYFCNTYYIMVLAWGFYLYVKSFETTLPLWA 170
QY 180 EC-----PVR-----NGSVAVVEAE--CEKSSATTVWYREADIDSDISBSGG 222
Db 171 TCGHTWNTPOCVFEIHRHEDCANGSLANTCDOLAEKRSVIEFWENKVLRSGLGVPGA 230
QY 223 LNKWMTCLLVWSITGGMAVGKIOSGKVMYFSSLPYVVLVACFLVRLGAVDGIIL 282
Db 231 LNWEVTLCLLACVLLVYFCVMKGVKSTGKIVYFTATFPYVVLVLLVRLVGLLPGALDGI 290
QY 283 HMFTEPKLKMPLDQVWREVATQVFFGLGLGFGGVIVFSSYNKONNCHFDGALVSFINFF 342
Db 291 YLKPDPWSKLSRSPQWIDAGTQIFFSYAIGLGTALGALSYNFRNNNNCYKDAIILALNSG 350
QY 343 TSVLATLVVVFVGLGFKANIMNEKCVVNAEKILGLYLTNTVLSRLDILPHVNFSLHTTKDY 402
Db 351 TSFFAGFVVFSLGFMA-----FEQG 371
QY 403 MEMDNVIMTKEDQFSAIGLDPCLLEDELDKSVQGTGLAFIAFTAMTHEFTSPFWSVME 462


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Db 372 VHISKV-----AESGGLAFTAYPRAVTLMPVAPLWAALF 406
QY 463 FLMLNLGLSGMTGAGITPIIDT-----SKVPKEMFTVGCCVTFELVGLLFVORSG 516
Db 407 FFMLLLGLDLSQFVGVEGFTGLDLLLPASYPRFQREISVALCCALCFVIDLSMVTDDG 466
QY 517 NYFVTMFDDYSATPLPLTLI--VILENIATAWIIYGPKKFMOELTEMLGFRPYRYFYMMKF 574
Db 467 MYVFOLEFYYSAS-GTLLWQAFWECVAVAWVYGADRFMDDIACMIGYRCPWKKWCWSP 525
QY 575 VSPPL-CMAVLTTASIIQLGVTPPAYSAWIKKEAAERYLYFPNPMALLITLIVVATLPIP 633
Db 526 FTPLVCMGIFIFNIY---YKPLVYN-----KTYVY-PWGEAMGWAFALSSMLCVP 573
QY 634 VVFLRHRHLL 644
Db 574 L-----HLL 577

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Search completed: April 21, 2003, 13:58:38
 Job time : 51 secs

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 13:57:53 ; Search time 22 seconds

(without alignments)
2498.695 Million cell updates/sec

Title: US-09-923-444A-2

Perfect score: 3817

Sequence: 1 MPKNSKVTQREHSSEHVTPES.....NPNPGYGRGYLLASTPESEL 727

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 75613885 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3817	100.0	727	10 US-09-923-444A-2	Sequence 2, Appli
2	2522.5	66.1	730	9 US-10-156-239-5	Sequence 5, Appli
3	2522.5	66.1	730	10 US-09-741-149-2	Sequence 2, Appli
4	2522.5	66.1	730	10 US-09-795-693-5	Sequence 5, Appli
5	2494	65.3	729	10 US-09-741-149-4	Sequence 4, Appli
6	1468.5	38.5	676	9 US-09-815-923-12	Sequence 12, Appli
7	1433	37.5	624	9 US-10-156-239-24	Sequence 24, Appli
8	1433	37.5	624	10 US-09-795-693-24	Sequence 24, Appli
9	1325	34.7	599	10 US-09-861-846-4	Sequence 4, Appli
10	1275	33.4	610	10 US-09-861-846-2	Sequence 2, Appli
11	1031.5	27.0	797	10 US-09-795-232-2	Sequence 2, Appli
12	937.5	24.6	630	10 US-09-843-598-10	Sequence 10, Appli
13	926.5	24.3	587	9 US-09-815-923-4	Sequence 4, Appli
14	924	24.2	622	10 US-09-843-598-11	Sequence 11, Appli
15	914	23.9	597	9 US-09-815-923-14	Sequence 14, Appli
16	892.5	23.4	727	9 US-09-815-923-10	Sequence 10, Appli
17	872	22.8	671	10 US-09-843-598-5	Sequence 5, Appli
18	868	22.7	671	10 US-09-843-598-7	Sequence 7, Appli
19	813.5	21.3	437	9 US-10-216-441-4	Sequence 4, Appli

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Sequence 6, Appli
Sequence 9, Appli
Sequence 4648, Ap
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Sequence 87, Appli
Sequence 43363, A
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Sequence 48618, A
Sequence 39755, A
Sequence 4, Appli
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Sequence 6, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 12626, A
Sequence 5281, Ap
Sequence 26, Appli
Sequence 26, Appli

20 813.5 21.3 437 10 US-09-818-656A-4
21 813.5 21.3 459 9 US-10-216-441-2
22 813.5 21.3 459 10 US-09-818-656A-2
23 763.5 20.0 556 9 US-09-815-923-6
24 674 17.7 421 10 US-09-843-598-9
25 506.5 13.3 579 9 US-09-738-626-4648
26 345.5 9.1 224 10 US-09-843-598-6
27 193.5 5.1 196 9 US-09-989-442-87
28 141 3.7 52 10 US-09-864-761-43363
29 126 3.3 151 9 US-09-989-442-101
30 122 3.2 672 9 US-09-928-530-5
31 122 3.2 672 9 US-10-162-012-30
32 115 3.0 1146 10 US-09-824-734-2
33 114 3.0 1503 9 US-10-007-706-1
34 111 2.9 49 10 US-09-864-761-48618
35 108.5 2.8 84 10 US-09-864-761-39755
36 108.5 2.8 1085 9 US-10-274-990-4
37 108.5 2.8 1085 10 US-09-734-674-4
38 106 2.8 563 10 US-09-915-181A-6
39 103.5 2.7 1032 10 US-09-728-137-8
40 103.5 2.7 1044 10 US-09-728-137-2
41 102.5 2.7 714 10 US-09-728-137-4
42 102 2.7 497 10 US-09-815-242-12626
43 100 2.6 469 10 US-09-815-242-5281
44 99.5 2.6 539 9 US-10-051-902-26
45 99.5 2.6 539 9 US-10-051-909-26

ALIGNMENTS

RESULT 1
US-09-923-444A-2
; Sequence 2, Application US/09923444A
; Patent No. US20020015980A1
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; FLEISCHMANN, ROBERT
; TITLE OF INVENTION: NEUROTRANSMITTER TRANSPORTER
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/923,444A
; FILING DATE: 08-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,815
; FILING DATE: 199-12-20
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele M. Wales
; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PF116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Db 539 LENIAVCFYVIGDKFEMEDLKDMLGFAPSYYYMYMYKISPLMLLSLLIASVWNGLSPPG 598
Qy 598 YSAWIKKEAAERYLYPPNPMALLITLIVVATLPIPVFVLRHFLHLLSDGS-NTLSVSYK 656
Db 599 YNAWIEDKASEFSLPTWGLVVCVSLVFAILPVFPVFLVRLENLDDSSGNLASVYK 658
Qy 657 KARMKMDISLENDETFRILSKVPSEAPSPMTHRSYLGPGSTSPLETSWNPNPGYGRG 716
Db 659 RGRVLKEPVNL-EGDDTSLIHGKIPSEMPSPNFGKNIYKQSGSPTLDTA--PNGRYIG 715
Qy 717 YLLA---STPESEL 727
Db 716 YLMADIMPDPESDL 730

RESULT 5
US-09-741-149-4
; Sequence 4, Application US/09741149
; Patent No. US20020031800A1
; GENERAL INFORMATION:
; APPLICANT: LI, Zhenya et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO00780
; CURRENT APPLICATION NUMBER: US/09/741,149
; CURRENT FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-741-149-4

Query Match 65.3%; Score 2494; DB 10; Length 729;
Best Local Similarity 64.0%; Pred. No. 1.6e-222;
Matches 471; Conservative 115; Mismatches 134; Indels 16; Gaps 9;

Qy 1 MPKNSKVTQREHSHSEHVETSVADLLALEPVD--YKQS--VLNVAGEAGKQKAVEEELD 56
Db 1 MPKNSKVVKRELDE-VIESVKDLLSNEDSADDAFKKSELIVDVEE---KQTDVVERSE 56

Qy 57 AED-RPANKSKLQYILAIGFSGVLGNINRFPYLCOKNGGAYLVPYLVLLIIIGIPLFF 115
Db 57 VKDARPAWNSKLOYLIAQVGSFGLGNVWRFPYLCOKNGGAYLLPYLLIIIGIPLFF 116

Qy 116 LELAVGQRIRRGISGVVHYICPRLGIGFSSCTIVCLFVGLYNYNVIIGWSIFEFKSFQYP 175
Db 117 LELSVGQRIRRGISGVVNTISPOLGGIGFASCVCFVVALYNYNVIIGWSLFFYSQSQFP 176

Qy 176 LPWSECPVVRNGSVAVAECEKSSATTYFWYREALDIDSISESGLNKMTLCLLVWV 235
Db 177 LPWDQCLPVKNASHTFVEPECEKSSATTYFWYREALNISTISESGLNKMTLCLLAAW 236

Qy 236 SIGGMVAGKGTQSSKVMYFSSLPFVYVUACFLVRGLLLRGAVDGLIHMFTPKLVKMLDP 295
Db 237 VVCLAMIKGTQSSKVMYFSSLPFVYVUACFLVRGLLLRGAVDGLIHMFTPKLVKMLDP 296

Qy 296 QWREAVATQVFFGLGFGGVVTFSSYNKDNCHFDGALVSFINFTSVLATLVVFFVL 355
Db 297 KWREAAQVFFALGFGGVVTFSSYNKDNCHFDGALVSFINFTSVLATLVVFFVL 356

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Qy 416 QFSAIGLDPCLLEDLKSVQGTGLAFTAMTHFTSPSPWSVNFLLMLNLGLGSMI 475
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Db 477 GTIEGIITPVVDTFVRKEILLTVICLLAFICLIPQVRSNGYFVTMFDYSATLPLLI 536
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Qy 596 PAYSAWIKKEAAERYLYPPNPMALLITLIVVATLPIPVFVLRHFLHLLSDGS-NTLSVS 654
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Qy 655 YKARMKMDISLENDETFRILSKVPSEAPSPMTHRSYLGPGSTSPLETSWNPNPGY 714
Db 657 YKGRVLEKPVNL-EGDDASLIHGKISSEMSPPNFGKNIYKQSGSPTLDTA--PNGRY 713
Qy 715 RGYLLA---STPESEL 727
Db 714 IGYLMADIMPDPESDL 729

RESULT 6

US-09-815-923-12

; Sequence 12, Application US/09815923

; Publication No. US20020197644A1

; GENERAL INFORMATION:

; APPLICANT: Gill, Sarjeet S.

; APPLICANT: Ross, Linda S.

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. US20020197644

; TITLE OF INVENTION: Target Sites for Insecticides

; FILE REFERENCE: 023070-093800US

; CURRENT APPLICATION NUMBER: US/09/815,923

; CURRENT FILING DATE: 2001-03-23

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 12

; LENGTH: 676

; TYPE: PRT

; ORGANISM: Manduca sexta

; FEATURE:

; OTHER INFORMATION: orphan transporter

US-09-815-923-12

Query Match 38.5%; Score 1468.5; DB 9; Length 676;

Best Local Similarity 44.8%; Pred. No. 1.9e-127;

Matches 291; Conservative 113; Mismatches 196; Indels 49; Gaps 11;

Qy 46 GKQAVEEELDAEDRPAWNSKLOYLIAQVGSFGLGNINRFPYLCOKNGGAYLVPYLV 105
Db 38 GSRGSLORDAPEEDRAAWSGKLQFFLSIIGYSVGLGNINRFPYLCQOQNGGAFPLPFLIM 97

Qy 106 LIITIGLFFLELAVGQRIRRGISGVVHYICPRLGIGFSSCTIVCLFVGLYNYNVIIGWSI 165
Db 98 LVLBSGILPLVLEMAIGOKMRLGSLGVWNTIHPWLGIGIGISSCVTLFVALYNYNVIITWVF 157

Qy 166 FYFPEKSFQY---PLPWSECPVVRNGSVAVAECEKSSATTYFWYREALDIDSISESG 222
Db 158 FYLENSIRLTADQLPWAHCP-YDNGT---AEAECNKASATYFWYREALDIDSISESG 213

Qy 223 LNKWMTLCLLVWISITGGMAVGKGTQSSKVMYFSSLPFVYVUACFLVRGLLLRGAVDGL 282
Db 214 PRWIVLYLLAWLIIVFIVMKGTQSSKVMYFSSLPFVYVUACFLVRGLLLRGAVDGL 273

Qy 283 HMTPTKLVKMLDPQWREAVATQVFFGLGFGGVVTFSSYNKDNCHFDGALVSFINFT 342
Db 274 HMYKPKLEKLDPTVWLDAAATQVYSFGLAFSGSLAFSGSNPPNNCVDRVLLSVSNAL 333

Qy 343 TSVLATLVVFFVLFKANKIMKECVVNAEKILGYLNTLSRDLIPPHV-NFSLHTTKD 401
Db 334 TAIYASVVIIFSLGFKAYTVVENCIVKEI-KVAL-----HHIGFTLNSTAD 380

Qy 402 YMENDNVIMTVKEDQF-----SALGLDPCLEDELKSVQGTGLAFTAMTHFT 453

Db 381 YY-----REQPRLNGTAALNLTGCTMSRQLEBAAGTGLAFIVTQAILKLT 430
QY 454 TSPWSVMEFLNLINLGLSMGTAGITPIIDT---SKVPKEMTVGCCVTFPLVGLL 510
Db 431 PAPFWSIIFLMLLSLUGSQIGMEGMLCTIPDIFFKRLSKPVITGVVCTCFVGLI 490
QY 511 FYQSGNFTVTFDDYSAFLPLTLIIVILENAVIAWYIGPKKFMQELTGMGERPYPFY 570
Db 491 FTTGAGEYWLKMFDSFAGTIGLVVALLKMAIVIIYIGHEKFTNDIYEMTGYRGIWQV 550
QY 571 MKFVSPCLMAVLTATSIITQGVTPPAYSAWIKKEAAERYLYPNPMALLITLIVVATL 630
Db 551 TWRYVGPALVTCILLSSVFLMNLNPNMYGAWNADEGRVTKTPYTWLVIAVLMILAGVL 610
QY 631 PIPVVEVLRRHLLS-----DGS-NTLSVSYKKARMKDISLENDE 672
Db 611 PIPVLLLRFFCLAFDVIDHOGSRRIETTVSTKEMNSDQDNVESSEE 659

RESULT 7

US-10-156-239-24

; Sequence 24, Application US/10156239

; Publication No. US20030036074A1

; GENERAL INFORMATION:

; APPLICANT: Glucksmann, Maria A.

; TITLE OF INVENTION: Kapeller-Libermann, Rosana

; TITLE OF INVENTION: NO. US20030036074A1el Nucleic Acid Sequences Encoding Human Trans

; TITLE OF INVENTION: ATPase Molecule, A Human Ubiquitin Conjugating Enzyme-Like Molecule, A Hu

; TITLE OF INVENTION: Ubiquitin Conjugating Enzyme-Like Molecule, and Uses Therefor

; FILE REFERENCE: 35800/247645

; CURRENT APPLICATION NUMBER: US/10/156,239

; CURRENT FILING DATE: 2002-05-24

; PRIOR APPLICATION NUMBER: 2002-05-24

; PRIOR FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 60/185,906

; PRIOR FILING DATE: 2000-02-29

; PRIOR APPLICATION NUMBER: 60/185,906

; PRIOR FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: 60/192,018

; PRIOR FILING DATE: 2000-03-24

; PRIOR APPLICATION NUMBER: 60/192,018

; PRIOR FILING DATE: 2001-03-14

; PRIOR APPLICATION NUMBER: 60/191,790

; PRIOR FILING DATE: 2000-03-24

; PRIOR APPLICATION NUMBER: 60/191,790

; PRIOR FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: 60/191,781

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 24

; LENGTH: 624

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Pfam consensus sequence

US-10-156-239-24

Query Match 37.5%; Score 1433; DB 9; Length 624;
Best Local Similarity 48.0%; Pred. No. 3.3e-124;
Matches 306; Conservative 95; Mismatches 18; Indels 54; Gaps 17;

QY 60 RPANNSKLQYTLAQIGFSGVGLNIWRFPYLCQKNGGGAYLVPLYLLIIIGIPFLPLELA 119
Db 1 RETWSGKLDVLSVVGFAVLGNWRFPYLCYKNGGGAFLLIPLIFLIVAGIPLPLELA 60
QY 120 VGORIRGSGIWHY-----ICPRGGIGFSSCIVCLFVGLYNNVIIGHSIYFFKS 171
Db 61 LGQYTRGSIIVWRKKILDKGICPLFKGIGYASIVAFYIGIYNNVIAWALYLFSS 120
QY 172 FOYPLPWSEC-----PVVRNGSVAVVEAE-----CEKSATYFWYREA 210
Db 121 FTTELWPATCNNSWNTPCNVEERENSTNGSLAALSSKNLTDYTLERTSPVEEFWERGV 180

QY 211 LDISDS--ISESGGNNKMTLCLLVVWSIGGMVAGKGIQS-SGKVMYFSSLFYVVLACF 267
Db 181 LKLSSESGTIDELGRLWELTCLLLAWIVVYFCLMKGVKSGSKVYVTFATFFYVVLIVL 240
QY 268 LVRGILLRGAVDGIILHMETPKLVKMLDPOVREVATOVFFGLGFGGGVIVFSSYNKQDN 327
Db 241 LIRGVTLPGAADGIKFYLTDPFSKLLDPOVWIDAATQIFSLGIGFGLVIALASYNKFNH 300
QY 328 NCHFDGALVSEINFETSVLATLVVVFVGLFKANIMKEKCVENAEKILGYLNTNVLSDRL 387
Db 301 NCYRDALIVSFINSITSLAGVIFVLSILGFMANIVQEQVPE-ENKILLSVLSRDL 356
QY 388 IPPHVNFSHLTKDYMENDNVMTKEDQFSALGDLDCILLEDEKSVSGTGLAFATFE 447
Db 357 I-PHVNLSALTA-DYSYVD-VISEVAESEF-VLGL--ACLEDELDKQVAGPLAFATPE 410
QY 448 AMTHFTPTSPFWSVMEFLMLINIGLSMGTAGITPIID----TSKVPKEMFTVCCCV 502
Db 411 AVTMLPLSPFWAVLEFLMLTLGLDSQFGVGEITALVDEFPILLRKVRRELLILLVCV 470
QY 503 FTELVLGLLVQSRGNFYVTMFDDYSAT-LPLTLIVILENAVIAWYIGPKKFMQELTMLG 561
Db 471 ISFLLGLFMVTEGGIYVFTLFDYAASGFSLLFVVFEECIAVAVWYIGIDRFYDDITEMLG 530
QY 562 FRPYRFYFMYMKFVSPCLMAVLTATSIITQGVTPPAYSAWIKKEAAERYLYPNPMALL 621
Db 531 FRPGLYKLCWKVSPLLILLFLIFISVOYGLKPLTYNNWIKKE--AEDYVY-PNWNALG 587
QY 622 ITLVVATPLPIPVVFLRHFHLLSDGNTLSVSYKKA 658
Db 588 WLLALSSMLCVPLYII---YKLLSTEGDSLLERLQKA 621

RESULT 8

US-09-795-693-24

; Sequence 24, Application US/09795693

; Patent No. US20020068710A1

; GENERAL INFORMATION:

; APPLICANT: Glucksmann, Maria A.

; TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and

; TITLE OF INVENTION: 32613, No. US20020068710A1el Human Transporters

; FILE REFERENCE: 35800/209292

; CURRENT APPLICATION NUMBER: US/09/795,693

; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 60/185,906

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 24

; LENGTH: 624

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Pfam consensus sequence

US-09-795-693-24

Query Match 37.5%; Score 1433; DB 10; Length 624;
Best Local Similarity 48.0%; Pred. No. 3.3e-124;
Matches 306; Conservative 95; Mismatches 18; Indels 54; Gaps 17;

QY 60 RPANNSKLQYTLAQIGFSGVGLNIWRFPYLCQKNGGGAYLVPLYLLIIIGIPFLPLELA 119
Db 1 RETWSGKLDVLSVVGFAVLGNWRFPYLCYKNGGGAFLLIPLIFLIVAGIPLPLELA 60
QY 120 VGORIRGSGIWHY-----ICPRGGIGFSSCIVCLFVGLYNNVIIGHSIYFFKS 171
Db 61 LGQYTRGSIIVWRKKILDKGICPLFKGIGYASIVAFYIGIYNNVIAWALYLFSS 120
QY 172 FOYPLPWSEC-----PVVRNGSVAVVEAE-----CEKSATYFWYREA 210
Db 121 FTTELWPATCNNSWNTPCNVEERENSTNGSLAALSSKNLTDYTLERTSPVEEFWERGV 180

QY 211 LDISDS--ISESGNLNWKMTCLLVVWSIGGMVAGKIQS-SGKVMYFSSLPYVWLACF 267
Db 181 LKLESSGIEDGERWELTCLLLAWIVYVFCMLKGVKSGSKGVYFTATFPVVLIVL 240
QY 268 LVRLGALLRGAVDGLHMFPPKLVKMLDPQVWREVATQVFFGLGFGGVIVFSSYNKODN 327
Db 241 LIRGVTLPGAADGIRKFLTPDFSKLLDPQWIDAATQIFPSGLGIGFVLIALASYNKPHN 300
QY 328 NCHFDGALVSFNFTSVTLATLVVFFVILGFKANIMNEKCVVENAEKILGYLNTNVLSD 387
Db 301 NCYDAIIVFSINITSIFLAGFVIFSLGFMANIVOEQGVPE--EKI--LLSVLSKDL 356
QY 388 IPPHNFSLHTKDXMEMDNVMTKEDQFSALGLDPCLEDELDKSVQGTGLAFIAFTE 447
Db 357 I-PHNVLSALTA-DYSVYD-VISEVAESER-VLGL--ACLEDELDKVAQAGFLAIYPE 410
QY 448 ANTHPTSPFWSVMFLMLNLGLSGMIGTMAITPIID-----TSKVPKEMFTVGC 502
Db 411 AVTMLPLSPFWALVFLMLTLGLDSQFGGVEGIITALVDEFPILLRKVRRELFIILVCV 470
QY 503 FTELVLGLLVQSRGNYVFTMEDYSAT-LPLTLVILENIAVAVIYGPKKFMOELTEMLG 561
Db 471 ISFLGLFNVTEGGIVYFTLDYASAGSLLFVFFECIAVAVYIDREYDDITTEMLG 530
QY 562 PRPYRYFYFMKFSVPLCMVLTASIIQLGVTPPAYSAWIKERAPERYLYFPNPMALL 621
Db 531 PRPGLYWKLCWKFVSPILLLELFFISIVQYGLKPLTYNNNIKE--AEDYVY-PNKANALG 587
QY 622 ITLVVATLPIPVVFLRHFLHLLSDGNTLSVSKKA 658
Db 588 WLLALSSMLCVPLYII---YKLLSTEGDSLLERLQKA 621

RESULT 9

US-09-861-846-4

; Sequence 4, Application US/09861846

; Patent No. US20020110852A1

; GENERAL INFORMATION:

; APPLICANT: GUEGLER, Karl et al.

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; FILE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL001065

; CURRENT APPLICATION NUMBER: US/09/861,846

; CURRENT FILING DATE: 2001-05-22

; PRIOR APPLICATION NUMBER: 09/752,821

; PRIOR FILING DATE: 2001-01-03

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0.

; SEQ ID NO 4

; LENGTH: 599

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-861-846-4

Query Match 34.7%; Score 1325; DB 10; Length 599;

Best Local Similarity 43.1%; Pred. No. 3.3e-114;

Matches 262; Conservative 115; Mismatches 191; Indels 40; Gaps 11;

QY 43 EAGGKQKAYEEELDAEDRPANWSKLOYIAQIGFSVGLGNWRFPYLCOKNGGGAYLV 102

Db 3 QASGMDPLVDIE---DERPKWDNKLQVLLSCIGFAVGLGNWRFPYLCQTHGGGAF 59

QY 103 LVLLIIIGIPLFLEAVGQIRRGSGVWHYICPRLGIGGFSFCVCLFVGLYNYVIAIG 162

Db 60 FIALVEGIPFLFYIELAIGRLRGSGVWKTISPYLGGVGLGCFVSFLVSLYNTVIL 119

QY 163 WSIFYFFKFSQYDPLPNSCECPVRNGSVAVAECEKSSATYFWYREALDIDSISESG 222

Db 120 WVLFFLNSFQPLPWPSTCLDNLRTGFV--QECQSGTSYFWYRQTLNITSDISNTGT 177

QY 223 LNKWMTLCLLVNVWSIGMAYGKIQSGSKVMYFSSLPYVWLACFLVRLGLLRGAVDGL 282

Db 178 IQKFLCLVACSWTVYLCVIRGIESTGKVIYFTALFPYLVLTIFLIRGLTLPGATEGLI 237
QY 283 HMFPTKLVKMLDPQVWREVATQVFFGLGFGGVIVFSSYNKODNCHDFDGLVSPINFE 342
Db 238 YLETPNNKTLQONPRVLDAAATQIFSLSLAFGGHIAFASYNPRNCKEADAVIALVNSM 297
QY 343 TSVLATLVVFLVGLGFKANIMNEKCVVENAEKILGYLNTNVLSDRLIPPHVNFSLHTTKDY 402
Db 298 TSLYASIAIFSVMGFKASNDYGRCLDRN---ILSLIN---EFDL--PELSIS---RD- 343
QY 403 MEMDNVMTKEDQ---FSAIGLDPCLLEDELDKSVQGTGLAFIAFTEAMTHPTSPFWS 459
Db 344 -EYPSVLMYLNATQARVAQLPLKCHLEDFDKSASGFLAFIVFTEAVLHMPGASVWS 402
QY 460 VMFELMLNLGLSGMIGTMAITPIID-----TSKVPKEMFTVGCCTFFLVGLLFPVORS 515
Db 403 VLEFGMLFTLGLSSMFCNMGCVITPLDMGILPKGIPKEVMTGVICFACFLSAICTLQS 462
QY 516 GNYFTVMDYDYSATPLTLVILENIAVAVIYGPKKFMOELTEMLGFRPYRYFYMWKFV 575
Db 463 GGYWLEIFDQFAASNLIIIFAFMEVGVVIHYGMKRFCDDEWMTGRRPGLYMQVTRVV 522
QY 576 SPLCMVLTASIIQLGVTPPAYSAW-----IKEEAARYLYFPNPMALLITLIVV 627
Db 523 SPMLFGIFUSYIVLLIQTTPPSYKAWNPQYEHFPPSREEK-----FYPGWVQVTCVLLSFL 577
QY 628 ATLPPIPV 635
Db 578 PSLWVPGV 585

RESULT 10

US-09-861-846-2

; Sequence 2, Application US/09861846

; Patent No. US20020110852A1

; GENERAL INFORMATION:

; APPLICANT: GUEGLER, Karl et al.

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; FILE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL001065

; CURRENT APPLICATION NUMBER: US/09/861,846

; CURRENT FILING DATE: 2001-05-22

; PRIOR APPLICATION NUMBER: 09/752,821

; PRIOR FILING DATE: 2001-01-03

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 610

; TYPE: PRT

; ORGANISM: Human

US-09-861-846-2

Query Match 33.4%; Score 1275; DB 10; Length 610;

Best Local Similarity 42.0%; Pred. No. 1.5e-109;

Matches 250; Conservative 111; Mismatches 190; Indels 44; Gaps 10;

QY 58 EDRPANWSKLOYIAQIGFSVGLGNWRFPYLCQNGGAYLVPLVLLIIGIPLFLE 117

Db 16 DERPKWDNKAQVLLSCIGFAVGLGNWRFPYLCQTYGGGAFILPYVIALVFEGIPFHV 75

QY 118 LAVGQIRRGSGVWHYICPRLGIGGFSFCVCLFVGLYNYVNIWGSIFYFFKFSQYPLP 177

Db 76 LAIGORLRKSGVWMTALSPYLSVGLGCVTLISFLISLYNITVAVWVLLNLSFQPLP 135

QY 178 WSECP--VVRNGSVAVVAECEKSSATYFWYREALDIDSISESGLNKMTLCCLLVW 235

Db 136 WSSCPDNLNRTGFV---EECQSSAVSYFWYRQTLNITADINDSGSIQWLLICLAAS 191

QY 236 SIGMAYGKIQSGSKVMYFSSLPYVWLACFLVRLGLLRGAVDGLIHMTPKLVKMLDP 295

Db 192 AVVMCMVIRGIETGKVIYFTALFPYLVLTIFLIRGLTLPGATKGLIYLFPPNNHILQNP 251

QY	345	VLATLVFVVVLGFKANIMNEKCVVNAEKILGYLNTNVLSDRLIPPHVNFSLHLLTKDYE	404
Db	373	FVSGFVIFVLYGMAERNED	393
QY	405	MDNVITWVKEDQFSALGLOPCLLEDELKSVOGTGLAFTAFTEAMTHPTSPFWSVMFFL	464
Db	394	-----VSEAVKD-----	429
QY	465	MLINLGLSGMIGTMAGITPIIDTSKVP-----KEMFTVGCVCVFTFLVGLLFFVORSQNY	518
Db	430	MLITLGLDSTFAGLEGVITAVLD-----EPHWAKRRERFVLAVVITCFGSLVTLFFGAY	487
QY	519	FVTMFDDYSATPLTLIVILENTAVAMIYGPKKFMQELTEMLGFRPYRYFYTMWKFVSP	578
Db	488	VKLLLEYATGPVALTVALIEAVASWFYIGITQFCRDVKEMLFGSPGNWCRICWVAISPL	547
QY	579	CMAVLTTASTIQLGVTPPAYSAWIKKEAAERYLYPPNWPMLLITLIVVATLIPVFWVL	638
Db	548	FLLEFI-----ICSLFPGPPQLRLF-----QYNY-PYNSIILCYCIGTSSFCICTIYAY	595
QY	639	RHFHLLSDGNTLSVSKYKARMKMDISNLEENDETRFILSKVPVSEAP	685
Db	596	R--LIITPGT-----FKERIUKSIT-----PEPTETIP	621

RESULT 13
 US-09-815-923-4
 ; Sequence 4, Application US/09815923
 ; Publication No. US20020197644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gill, Sarjeet S.
 ; APPLICANT: Ross, Linda S.
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. US20020197644A1e1
 ; TITLE OF INVENTION: Target Sites for Insecticides
 ; FILE REFERENCE: 023070-093800US
 ; CURRENT APPLICATION NUMBER: US/09/815,923
 ; CURRENT FILING DATE: 2001-03-23
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 587
 ; TYPE: PRT
 ; ORGANISM: Manduca sexta
 ; FEATURE:
 ; OTHER INFORMATION: serotonin transporter
 ; US-09-815-923-4

Query Match	24.38;	Score	926.5;	DB	9;	Length	587;
Best Local Similarity	31.59;	Pred. No.	2.9e-77;				
Matches	203;	Conservative	131;	Mismatches	208;	Indels	103;
Gaps	14;						
Qy	47	KOKAVEEL-DAEDRPAMNSKLQILTAIGFSGVLGNWRFPYLCQKNGGAYLVPYLVL	105				
Db	24	KRSVSVSLTPARQRETWAKKAELLAVGFAVDLGNVWRFPYICYQNGGAFLIPYCVM	83				
Qy	106	LIITGIPFFLEAVGORIRGSGTGVWHYICPRGGIGFSSCIYCLFVGLVYNYVITGWSI	165				
Db	84	LLFGGLPFFLEALGQVHRCGCLTLWKRICPALKGVGTAICMDIYMGMYNTIIGWAV	143				
Qy	166	VYF---FKSFQVPLPWSCEPVPVRNGSVA--VVEAECEKSSAT--TYFYWYREALD--ISDS	216				
Db	144	YYLIATLASINSVLPWTCSDNEWNTPLCTPVTSPQTNPNSSTPAKEFFERNVLEQHKSG	203				
Qy	217	ISESGGLNWKMTCLLLVWVSIGGMVAGKGIQSSGKVMYFSSLFPVXVLACELVRCGLLRG	276				
Db	204	LDDMGPIKPSALCALCVGFVFLVYFSLWKGVRSGAKGVWTAIAPVLIILLARGVTLPG	263				
Qy	277	AVDGTILHMTFPLKVRMLDPQVMREYATQVFFGLGLGFGGVIVFSSYNKQDNCHFDGALV	336				
Db	264	ATEGYRYLTPPEWHKLONSKVMIDAASQIFSLGSGFGFTLLASSLYSNFNNNCYRDALIT	323				

[illegible]

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RESULT 14
US-09-843-598-11
; Sequence 11, Application US/09843598
; Patent No. US20020010944A1
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Ranganathan, Rajesh
; TITLE OF INVENTION: CESTR GENES, PROTEINS, AND MODULATORY
; TITLE OF INVENTION: COMPOUNDS
; FILE REFERENCE: 01997/525002
; CURRENT APPLICATION NUMBER: US/09/843.598
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/200,549
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-843-598-11

```

Query Match	24.2%	Score 924;	DB 10;	Length 622;
Best Local Similarity	31.2%	Pred. No. 5.4e-77;		
Matches	Conservative 117;	Mismatches 228;	Indels 108;	Gaps 11;

QY	4	NSKVTOREHSSEHVTES-VADLLALEEPVDYKQSVLNVAGEAGGKOKKAVEEELDAEDRPA	62
DB	32	NNEDDSNEDGDHPTPAKVTDPL-----APKLANNERILVVSVTERRET	76
QY	63	WNSKLOYILAQIGFSVGLGNTRPPEYLCQKNGGAYLVPLYVLLIIIGIPFLFLELAVGQ	122
DB	77	WGQKAPELLAVIGFAVDLGNVWRPPYICVQNGGGAFLVPYCLPIEFGGLPLFYEMELAQQ	136
QY	123	RIRGSLGVWHYICPRLGGIGFSSICVLFCVLGYNVNIIIGWSIFYEPKSPQYPLPWSEC-	181
DB	137	FHRGCGLSIKWRICPALKGVYAICLIDIMGYNYNIIIGWVYIFYASTSKLPWTSCD	196
QY	182	-PVPVRNGSVAAVEACEK--SSATYFWFYREALDI--SDSISPSGGNNWMTLCLLVYWS	236
DB	197	NPNTENCMQVTSNFTELATSPAKEFFPERKVLSEYKGNGLDFMGVPVKPTLALCVFGVEV	256
QY	237	IGGMVAGCKGTOSSKWNYSFSSLPVYVVLACFLVRGLLLRGAVDGIILHMFPTPKLYKMLDPQ	296
DB	257	LVYFSLWKGVRSAGKVVWMTALAPYVWVLIILVRGVSPLGCADEGKIYLLTPEWHKLNKSK	316
QY	297	VWREVAQTQVFGLGFGGVIVFYSSNYKODNNCHFDGALVSFTNFTSVLZLTLVVFVVLG	356

Db 317 VIDAASQIFSLGPGFTLLALSYNNKNNCYRDALITSSINCLTSFLAGFVIFSLG 376
QY 357 FKANINNEKCVVENAEKILGVLNTNVLSDLPHPHNFSLTTTKDYMEDNDVIMTVK 416
Db 377 YMAVQ-----EQRPAEV- 369
QY 417 FSALGLDPCLEDELDK-SVOGTGLAFIAFTAMTHPTSPFWSVMFFLMLINLGLSG 475
Db 383 -----KVSIDKVGLEGCLVIVPEATATWSGVSFWSLIFLMLITGLDSTF 431
QY 476 GTMAGITPTIID-----KEMFTVGCCTFELVGLFVQSGNYFVTMDDYSAT 529
Db 432 GLEAMITALCD--EYPRVIGRRRELEFVLLILAEIFLCALPTMTYGGVVLNVLNVP 489
QY 530 LPTLIVILENIAVAVIYGPKEQELTEMLGFRPYFYFMMKFVSPCLMAVLTTAS 587
Db 490 LALFVVEAGVWFYGVDRSSDVEQMLGSKPGLFWRICWTYIISPVFLITIFISIM 549
QY 590 QLGVTTPAYSATWKEEAERYLYFPNPMALLITLIVVATLPIPVVFLRHFHLLSDG 647
Db 550 -----GYKEMLGEY-YYPDWSYQVGNVATCSSLVCLIPMYIYKFFASKG 595

RESULT 15

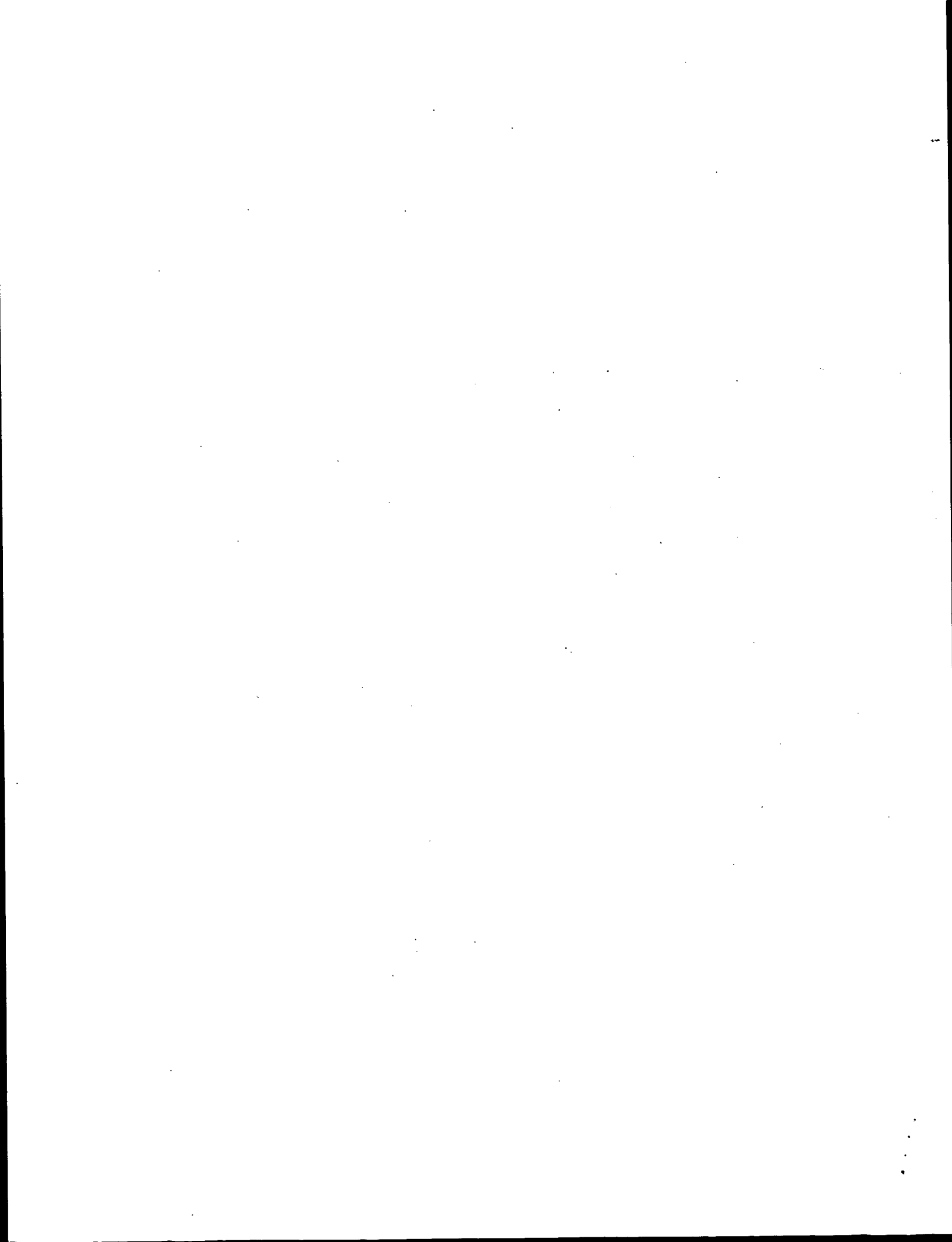
US-09-815-923-14
; Sequence 14, Application US/09815923
; Publication No. US20020197644A1
; GENERAL INFORMATION:
; APPLICANT: Gill, Sarjeet S.
; APPLICANT: Ross, Linda S.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. US20020197644A1
; FILE OF INVENTION: Target Sites for Insecticides
; FILE REFERENCE: 023070-093800US
; CURRENT APPLICATION NUMBER: US/09/815, 923
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Manduca sexta
; FEATURE:
; OTHER INFORMATION: GABA transporter
US-09-815-923-14

Query Match 23.9%; Score 914; DB 9; Length 597;
Best Local Similarity 29.7%; Pred. No. 4.3e-76;
Matches 205; Conservative 122; Mismatches 217; Indels 146; Gaps 15;

QY 27 LEEPVDYKQSVNLVAGE-AGGQKQAVEEELDAEDRPAWNSKIQYLLAQIGFSVGLGNWR 85
Db 1 METKNDSRDDIELSAQSGSNKPSDVAVKSNLPERGSKLDFILSVIGLAIGLGNVR 60
QY 86 FPYLCQKNGGAYLYPYLVLLIIGIPLEFLAVQRRRGSGIGVWHYICPRLGGIFS 145
Db 61 FPYLCYKNGGAFILPYFLTLFLAGIPMFELAMGQMLTIGLGVFK-IAPIFKGIGYA 119
QY 146 SCIVCLFVGLVYVNIIGNSIFYFFKSFQYPLPSECPPV----- 184
Db 120 AAVSWCMWVYIVILAWAIFYFFNSMRSDVPMRCDNYNTATCVNPDYDRKNLTCWSSL 179
QY 185 -----RNGSVAVVEACEKSSATYFYREALDISISGGLNKMWTCLLV 233
Db 180 GDMSTFCFLNGRNVSKAVL-----SDPVKEFWERRALQISSGIEHIGNIRWELAGTLL 233
QY 234 VWSIGGMVAVGKIQSGKVMVFFSLFPYVVLACFLVRGLLRCAVDGILLHMTPLKVKML 293
Db 234 VVLCYFCIKWGVRTGKVVFTALFPFLTLVIRGITLPGAMEGKIKFYVMPNMSKLL 293
QY 294 DPQWREVATQVFFGLGFGGVIYFSSYNKQDNNCHFDGALVSFINFTTSVLTALVWF 353
Db 294 ESEWIDAVTQIFFSYGLGLGLTVALGYSNKNFTNNVYKDALIVCSVNSSTSMFAGFVFS 353

QY 354 VLGFKANINNEKCVVENAEKILGVLNTNVLSDLPHPHNFSLTTTKDYMEDNDVIMTVK 413
Db 354 VVGFMH-----EQRPAEV- 369
QY 414 EDOFSALGLDPCLEDELDK-SVOGTGLAFIAFTAMTHPTSPFWSVMFFLMLINLGLSG 473
Db 370 -----AASGPGLAFLAYPSAVLQPLGAPLWNSCLFFEFMLLLIGLDS 409
QY 474 MGMTMAGITPTIID-----TSKVPKEMFTVGCCTFELVGLFVQSGNYFVTMDDYSAT 529
Db 410 QCTMEGFTAVIDENWPKLLRRRKEIFAIATCIIISYLVGLSCISEGGMYVFOILDSYAVS 469
QY 530 -LPTLIVILENIAVAVIYGPKEQELTEMLGFRPYFYFMMKFVSPCLMAVLTTAS 587
Db 470 GFCLLFLIFECVSIWAFGVNRFYDGIKEMIGYIPTIMWKFVWGTTPAICISVF-IFN 528
QY 588 LIQLGVTTPAYSATWKEEAERYLYFPNPMAL--LITLIVVATLPIPVVFLR----- 639
Db 529 LVQW--TPIKYMY-----EYPWWSHAFGWFTALSSMLCIPGYMIYLWRVTPGTW 576
QY 640 --HFHLLSDGSNTLSYSYKKARMKDISNL 667
Db 577 QEKFH-----KIVRIPEDVPSL 593

Search completed: April 21, 2003, 14:03:04
Job time : 25 secs



Db 1 MPKNSKVTQREHSEHVSADLLALEPVDYKQSVLNAGEAGGKQKAVEEELDAEDR 60
Qy 61 PAWSKLOVLAQIGSVGLNWRFPYLCOKNGGGAYLPYLVLLIIIGIPLFFLEAV 120
Db 61 PAWSKLOVLAQIGSVGLNWRFPYLCOKNGGGAYLPYLVLLIIIGIPLFFLEAV 120
Qy 121 GQIRRGSGVWHYICPRLGIGFSSCI VCLFVGLYNNVIGWSIFYFFKSFQYPLPWS 180
Db 121 GQIRRGSGVWHYICPRLGIGFSSCI VCLFVGLYNNVIGWSIFYFFKSFQYPLPWS 180
Qy 181 CPVVRNGSVAVVAEAECEKSSATYFWYREALDIDSISSESGGLNWKMTCLLVVWSIGGM 240
Db 181 CPVVRNGSVAVVAEAECEKSSATYFWYREALDIDSISSESGGLNWKMTCLLVVWSIGGM 240
Qy 241 AVKGIGQSGKVMYFSSLPYVACFLVRGLLRGAVDGLHMFTPKLVKMLDPQVWRE 300
Db 241 AVKGIGQSGKVMYFSSLPYVACFLVRGLLRGAVDGLHMFTPKLVKMLDPQVWRE 300
Qy 301 VATQVFFGLGFGGVIVFSSYNKQDNCHFDGALVSFINFTSVLATLVVVFVGLGFKAN 360
Db 301 VATQVFFGLGFGGVIVFSSYNKQDNCHFDGALVSFINFTSVLATLVVVFVGLGFKAN 360
Qy 361 IMNEKCVVENAEKILGYLNTNLSRDLIPPHVNFSLTTKDYMEMDNVIMTVKEDQFSAL 420
Db 361 IMNEKCVVENAEKILGYLNTNLSRDLIPPHVNFSLTTKDYMEMDNVIMTVKEDQFSAL 420
Qy 421 GLDPCLEDELKSVQGTGLAFIAFTTEAMTHFTSPFWSVFFLMLINLGLSGMIGTMAG 480
Db 421 GLDPCLEDELKSVQGTGLAFIAFTTEAMTHFTSPFWSVFFLMLINLGLSGMIGTMAG 480
Qy 481 ITTPIIDTSKVPKEMFTVCCVFTFLVGLLFVQSRGNYFVTFMEDDYSATLPLTLIVILEN 540
Db 481 ITTPIIDTSKVPKEMFTVCCVFTFLVGLLFVQSRGNYFVTFMEDDYSATLPLTLIVILEN 540
Qy 541 IAVAWIYGPKKMQELTEMLGPRPYRFYFWMKRFVSPCLMAVLTTASIIQLGVTPPAYSA 600
Db 541 IAVAWIYGPKKMQELTEMLGPRPYRFYFWMKRFVSPCLMAVLTTASIIQLGVTPPAYSA 600
Qy 601 WKEEAERYLYFPNPMALLITLIVVATLPIPVVFLRHFHLLSDGNTLSVSKKARM 660
Db 601 WKEEAERYLYFPNPMALLITLIVVATLPIPVVFLRHFHLLSDGNTLSVSKKARM 660
Qy 661 MKDISNLEENDETRFILSKVPSEAPSPMTHRSYLGPGSTSPLETSWNPNPGYGRGYLLA 720
Db 661 MKDISNLEENDETRFILSKVPSEAPSPMTHRSYLGPGSTSPLETSWNPNPGYGRGYLLA 720

RESULT 2
PCT-US94-05363A-2
; Sequence 2, Application PC/TUS9405363A
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Neurotransmitter Transporter
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05363A

; FILING DATE: SUBMITTED HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; PCT-US94-05363A-2

Query Match 99.6%; Score 3803; DB 5; Length 727;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 725; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MPKNSKVTQREHSEHVSADLLALEPVDYKQSVLNAGEAGGKQKAVEEELDAEDR 60

Db 1 MPKNSKVTQREHSEHVSADLLALEPVDYKQSVLNAGEAGGKQKAVEEELDAEDR 60

Qy 61 PAWSKLOVLAQIGSVGLNWRFPYLCOKNGGGAYLPYLVLLIIIGIPLFFLEAV 120

Db 61 PAWSKLOVLAQIGSVGLNWRFPYLCOKNGGGAYLPYLVLLIIIGIPLFFLEAV 120

Qy 121 GQIRRGSGVWHYICPRLGIGFSSCI VCLFVGLYNNVIGWSIFYFFKSFQYPLPWS 180

Db 121 GQIRRGSGVWHYICPRLGIGFSSCI VCLFVGLYNNVIGWSIFYFFKSFQYPLPWS 180

Qy 181 CPVVRNGSVAVVAEAECEKSSATYFWYREALDIDSISSESGGLNWKMTCLLVVWSIGGM 240

Db 181 CPVVRNGSVAVVAEAECEKSSATYFWYREALDIDSISSESGGLNWKMTCLLVVWSIGGM 240

Qy 241 AVKGIGQSGKVMYFSSLPYVACFLVRGLLRGAVDGLHMFTPKLVKMLDPQVWRE 300

Db 241 AVKGIGQSGKVMYFSSLPYVACFLVRGLLRGAVDGLHMFTPKLVKMLDPQVWRE 300

Qy 301 VATQVFFGLGFGGVIVFSSYNKQDNCHFDGALVSFINFTSVLATLVVVFVGLGFKAN 360

Db 301 VATQVFFGLGFGGVIVFSSYNKQDNCHFDGALVSFINFTSVLATLVVVFVGLGFKAN 360

Qy 361 IMNEKCVVENAEKILGYLNTNLSRDLIPPHVNFSLTTKDYMEMDNVIMTVKEDQFSAL 420

Db 361 IMNEKCVVENAEKILGYLNTNLSRDLIPPHVNFSLTTKDYMEMDNVIMTVKEDQFSAL 420

Qy 421 GLDPCLEDELKSVQGTGLAFIAFTTEAMTHFTSPFWSVFFLMLINLGLSGMIGTMAG 480

Db 421 GLDPCLEDELKSVQGTGLAFIAFTTEAMTHFTSPFWSVFFLMLINLGLSGMIGTMAG 480

Qy 481 ITTPIIDTSKVPKEMFTVCCVFTFLVGLLFVQSRGNYFVTFMEDDYSATLPLTLIVILEN 540

Db 481 ITTPIIDTSKVPKEMFTVCCVFTFLVGLLFVQSRGNYFVTFMEDDYSATLPLTLIVILEN 540

Qy 541 IAVAWIYGPKKMQELTEMLGPRPYRFYFWMKRFVSPCLMAVLTTASIIQLGVTPPAYSA 600

Db 541 IAVAWIYGPKKMQELTEMLGPRPYRFYFWMKRFVSPCLMAVLTTASIIQLGVTPPAYSA 600

Qy 601 WKEEAERYLYFPNPMALLITLIVVATLPIPVVFLRHFHLLSDGNTLSVSKKARM 660

Db 601 WKEEAERYLYFPNPMALLITLIVVATLPIPVVFLRHFHLLSDGNTLSVSKKARM 660

Qy 661 MKDISNLEENDETRFILSKVPSEAPSPMTHRSYLGPGSTSPLETSWNPNPGYGRGYLLA 720

Db 661 MKDISNLEENDETRFILSKVPSEAPSPMTHRSYLGPGSTSPLETSWNPNPGYGRGYLLA 720

QY 721 STPESEL 727
Db 721 STPESEL 727

RESULT 3
US-08-149-100-2
; Sequence 2, Application US/08149100
; Patent No. 5559021
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli E.
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A NOVEL MAMMALIAN
; TITLE OF INVENTION: TRANSPORTER HOMOLOGOUS TO NEUROTRANSMITTER TRANSPORTERS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,100
; FILING DATE: 08-NOV-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44744/JPW/TEP
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 6640525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 616 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-149-100-2

Query Match 34.1%; Score 1302.5; DB 1; Length 616;
Best Local Similarity 43.1%; Pred. No. 1.3e-119;
Matches 265; Conservative 122; Mismatches 191; Indels 37; Gaps 14;
QY 38 LNVAGBAGKQKAVEELDAED---RPAWNSKIQYLAIGFSGVGLGNTWRFPYLCQKN 93
Db 3 LAIKRASKQRPDEKARDMEKARPQWGNLQFVFCISAVGLGNVWRFPYLCOMY 62
QY 94 GGGAYLVPLVLIIGIPFLFLELAVGQRIRSGIGWHYICPRLGGIGFSSICVLFFV 153
Db 63 GGGSLVPLVLIIGIPFLFLELAVGQRIRSGIGWHYICPRLGGIGFSSICVLFFV 122
QY 154 GLYXNVIIQWSIFYPFKSFQYPLPWSECPVVRNGSVAVVAEAEKSSATYFWYREALDI 213
Db 123 SMYINVINAWGFWYLFHSFDPLPWSVCPPL--NSNRTGYDECEKASQYFWYRKTLNI 180
QY 214 SDSISGGLNRMKMTLCILVWSIGGMVAGKIQSSGMVGFSSLPYVVLVACLPLVRLGL 273
Db 181 SPSIQENGQVQWEPALCLTLAWLVYLCILRTGTESTGKVYFTALMPYCVLIYLVRLGL 240
QY 274 LRQAVDGIHMTFPLKVLKMLDPQVWRVATQVFFGLGFGVGVVFSYKQDNCHFDG 333
Db 241 LHGATNGLMYMTPKTEQLANPRAWINAATQIFFSLGLGFGSLIAFASYNPSNDCQKHA 300
QY 334 ALVSFINFTSVLTLVVFVVLGFGKAIMNKECVVENAEKILGVLNTNVLNRDLIPPHVN 393

Db 301 VIVVINSSTISFASIVTFYSIYGKATFNENCL-----NKVI-LLLTN--SFDL-----E 348
QY 394 FSHLTTRKDYMEMDNVIMTVKEDQFSAF--GLDPCLLEDELDKSVQGTGLAFIAFTEAMTH 451
Db 349 DGFLTASNLEEVKDYLASTYPNKYSEVFPPIRNCSELELNTAVQGTGLAFIVYAEAIKN 408
QY 452 FTSPTFSWVFFLMLINLGLSGMIGTWAGITTPID----TSKVPKEMFTVGCCTVFFELV 507
Db 409 MEVSQLSWVLYFFMLLMGLMGSMGLNTAAITPLTDSKVISSYLPKKAISGLVCLINCAV 468
QY 508 GLLFVQSGNYFVTMFDDYSATPLTLIVILENTAVAWIYGPCKFMQELTMLGPRPRF 567
Db 469 GWFTWEAGNYWFDINDYATLISLLIVLIVETIACVYVGLRRFESDLRMTG-RPLNW 527
QY 568 YF-YMKKFVSPLC---MAVLTASIIQLGVTTPPAYSAWIKKEAAERYLYFFNWP---MAL 620
Db 528 YMKAMWAFVSPLLIIGLFIYLSYILTGL--QYQAW---DATQGLVTKDYPPHALAV 582
QY 621 LITLIVVATLPIPVV 635
Db 583 IGLLVASTMCIPLV 597

RESULT 4
US-08-700-013B-19
; Sequence 19, Application US/08700013B
; Patent No. 5919653
; GENERAL INFORMATION:
; APPLICANT: Albert, Vivian R.
; APPLICANT: Kowalski, Leslie R.Z.
; APPLICANT: Borden, Laurence A.
; APPLICANT: McKelvy, Jeffrey F.
; TITLE OF INVENTION: Human Glycine Transporter
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,013B
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-700-013B-19

Query Match 27.2%; Score 1036.5; DB 2; Length 797;
Best Local Similarity 34.0%; Pred. No. 3.3e-93;
Matches 223; Conservative 111; Mismatches 186; Indels 135; Gaps 14;

QY 36 SVLNVA---GEAGGKOKAVEEELDAEDRPAWNSKLOVILAOIGFSVGLGNWRFPYLCOK 92
DB 173 SVATVATQDEQDENKA-----RGWSSKLDLFILSVGVAVGLGNWRFPYLAQ 223
QY 93 NGGAYLVPYLVLLIIIGIPLFFLEAVGORIRRGSGVWHYICPRGGIGFSSCIVOLF 152
DB 224 NGGAFILPYLMLALAGLPIFFLEVSLGOFASQGPVSVNKA1-PALQGGCIAMLIISVL 282
QY 153 VGLYNNVIIGWSIFFFKFSQPLPSEC-----PVVR-- 185
DB 283 IAIYNNVIICYTLFYLFAFVSFLPWGSCNNPNTPECKDKTKLLDSCVLSHDPKIQIK 342
QY 186 -----NGSVAVVEACEK---SSATTYFWYREALDISDSISBSGGLNWKMTLCLL 232
DB 343 NSTFCMTAYPNVTMNTFSQANKTFVSGSEYFKY-FVLKISAGIEYGEIRWPLALCLF 401
QY 233 VWSIGGMAYGKIGSSGKVMYFSSLPYVVLACFLVRLGALLRGAVDGLHMFPTPKLVKM 292
DB 402 LAWVIYASLAKGIKTSKGVVYFATPPYVVLVILLIRGVTLPAGAGIWIYFIPKWEKL 461
QY 293 LDQVWREAVATQFFGLGFGGVIVFSSYNKODNCHDFGALVSFNFSTSLATLVVF 352
DB 462 TDAVWMDAATQFFLSAAGGLITLSSYNKFNHNCYRDTLIVTCTNSATSIAGFVIF 521
QY 353 VVLGFKANIMNEKCVVENAEKILGYLNTNVLSDRLIPPHVNFSLHTTKDYMENDNVMIV 412
DB 522 SVIGFMAN--ERKVNIENTV----- 538
QY 413 KEDQFSALGDLPCLEDELKSVQGTGLAFIATFAMTHPTSPFWSVMFFMLNLGLG 472
DB 539 -----ADQGGIAFVYVPEALTRPLSPFWAIIFFLMLLTGLD 577
QY 473 SMIGTMAGITPIIDT---SKVPKEMFTVGCCTFVLVGLLFVQSRGNYFVTMFDYSA 528
DB 578 TMFATIEIVTSISDEFPKYLTHKPVFTLGCCICFFINGFPMTQGGIYMFQVDTYAA 637
QY 529 TLPLTLIVILENIAVAMYGPKFMQELTEMLGFRPYRYFYFYMVKFVSPCLMAVLTASI 588
DB 638 SYALVILAIFFELVIGSVYGLQRCFEDIEMMIGFQPNIFWKVCWAFVTPITLTILFCFSF 697
QY 589 IOLGVTTPPAYSAWIKKEAERYLYFPNPMALLITLIVVATLPPIPVVFLRHFHL 643
DB 698 YQW--EPMTYGSY-----RY---PNWSMVLGWLMLACSVIWIPIIMEVIK-MHL 739

RESULT 5
US-09-191-468-124
; Sequence 124, Application US/09191468A
; Patent No. 6416975
; GENERAL INFORMATION:
; APPLICANT: Gallagher, Michael J.
; APPLICANT: Burgess, Loyd R.
; APPLICANT: Brunden, Kurt R.
; TITLE OF INVENTION: Human Glycine Transporter Type 2
; FILE REFERENCE: 12311US01
; CURRENT APPLICATION NUMBER: US/09/191,468A
; CURRENT FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 124
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Human
US-09-191-468-124
Query Match
Best Local Similarity 34.08; Pred. No. 3.3e-93;
Matches 223; Conservative 111; Mismatches 186; Indels 135; Gaps 14;
QY 36 SVLNVA---GEAGGKOKAVEEELDAEDRPAWNSKLOVILAOIGFSVGLGNWRFPYLCOK 92
DB 173 SVATVATQDEQDENKA-----RGWSSKLDLFILSVGVAVGLGNWRFPYLAQ 223

QY 93 NGGAYLVPYLVLLIIIGIPLFFLEAVGORIRRGSGVWHYICPRGGIGFSSCIVOLF 152
DB 224 NGGAFILPYLMLALAGLPIFFLEVSLGOFASQGPVSVNKA1-PALQGGCIAMLIISVL 282
QY 153 VGLYNNVIIGWSIFFFKFSQPLPSEC-----PVVR-- 185
DB 283 IAIYNNVIICYTLFYLFAFVSFLPWGSCNNPNTPECKDKTKLLDSCVLSHDPKIQIK 342
QY 186 -----NGSVAVVEACEK---SSATTYFWYREALDISDSISBSGGLNWKMTLCLL 232
DB 343 NSTFCMTAYPNVTMNTFSQANKTFVSGSEYFKY-FVLKISAGIEYGEIRWPLALCLF 401
QY 233 VWSIGGMAYGKIGSSGKVMYFSSLPYVVLACFLVRLGALLRGAVDGLHMFPTPKLVKM 292
DB 402 LAWVIYASLAKGIKTSKGVVYFATPPYVVLVILLIRGVTLPAGAGIWIYFIPKWEKL 461
QY 293 LDQVWREAVATQFFGLGFGGVIVFSSYNKODNCHDFGALVSFNFSTSLATLVVF 352
DB 462 TDAVWMDAATQFFLSAAGGLITLSSYNKFNHNCYRDTLIVTCTNSATSIAGFVIF 521
QY 353 VVLGFKANIMNEKCVVENAEKILGYLNTNVLSDRLIPPHVNFSLHTTKDYMENDNVMIV 412
DB 522 SVIGFMAN--ERKVNIENTV----- 538
QY 413 KEDQFSALGDLPCLEDELKSVQGTGLAFIATFAMTHPTSPFWSVMFFMLNLGLG 472
DB 539 -----ADQGGIAFVYVPEALTRPLSPFWAIIFFLMLLTGLD 577
QY 473 SMIGTMAGITPIIDT---SKVPKEMFTVGCCTFVLVGLLFVQSRGNYFVTMFDYSA 528
DB 578 TMFATIEIVTSISDEFPKYLTHKPVFTLGCCICFFINGFPMTQGGIYMFQVDTYAA 637
QY 529 TLPLTLIVILENIAVAMYGPKFMQELTEMLGFRPYRYFYFYMVKFVSPCLMAVLTASI 588
DB 638 SYALVILAIFFELVIGSVYGLQRCFEDIEMMIGFQPNIFWKVCWAFVTPITLTILFCFSF 697
QY 589 IOLGVTTPPAYSAWIKKEAERYLYFPNPMALLITLIVVATLPPIPVVFLRHFHL 643
DB 698 YQW--EPMTYGSY-----RY---PNWSMVLGWLMLACSVIWIPIIMEVIK-MHL 739

RESULT 6
US-08-700-013B-21
; Sequence 21, Application US/08700013B
; Patent No. 5919653
; GENERAL INFORMATION:
; APPLICANT: Albert, Vivian R.
; APPLICANT: Kowalski, Leslie R.Z.
; APPLICANT: Borden, Laurence A.
; APPLICANT: McKelvy, Jeffrey F.
; TITLE OF INVENTION: Human Glycine Transporter
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,013B
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

RESULT 8
US-09-795-232-2

; TITLE OF INVENTION: Human Glycine Transporter
 ; NUMBER OF SEQUENCES: 41
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dechert Price & Rhoads
 ; STREET: 997 Lenox Drive, Building 3, Suite 210
 ; CITY: Lawrenceville
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08543
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700,013B
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bloom, Allen
 ; REGISTRATION NUMBER: 29,135
 ; REFERENCE/DOCKET NUMBER: 317743-108
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 609-520-3214
 ; TELEFAX: 609-520-3259
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 27:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 799 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-700-013B-27

Query Match 26.9%; Score 1028; DB 2; Length 799;
 Best Local Similarity 32.2%; Pred. No. 2.3e-92;
 Matches 228; Conservative 118; Mismatches 208; Indels 154; Gaps 16;
 QY 43 EAGGKQKAVEEELDAEDPAWNSKLOYILAOIGFSGVLGNWFFPFLCOKNGGGAYLVPI 102
 DB 195 EGGDKNA-----RGNWSSKLDLILSMVGAVGLGNWVRFPYLAFOGNGGAFILPI 235
 QY 103 LVLLIIIGIPLFLEAVGQRIIRGSGIGVWHYICPRLGGIGFSSCIVCLFVGLYNNVIIG 162
 DB 236 LMLALAGLPIFFLEVLGQFASQGPVSVWKAI-PALQCGGIAMLIISVLIAIYNNVIIC 294
 QY 163 WSIFFKFSQYPLPWSEC-----PVR----- 185
 DB 295 YTLFYLASFVSFLPWGSCNNPNTPECKDKTKLLDSCVIGDHPKIQIKNSTFCMTAYP 354
 QY 186 NGSAVVAEAECK-----SSATTYFWYREALDISDSISESGLANWMTLCLLVVWSIGMAV 242
 DB 355 NLTMVNTFSQANKTFVSGSEEFKY-FVLKISAGIEYPCGIRWPLPFCLFLAWIIVYASL 413
 QY 243 KGIOSSGKVMYFSSLPYVVLACFLVRLGALLRGAVDGIHMTPTKLVKMLDPQVWREVA 302
 DB 414 AKGIKTSKVYVFTATFPYVVLVILLIRGVTLPAGAGIWIYFITPKWEKLTDAVWKDAA 473
 QY 303 TVQVFGGLGFGGVIVFSSYNKQDNCHFDGALVSEINFSTVSLATLVFVGLFKANIM 362
 DB 474 TOIFPFLSAAGWGLLTLSSYNKFNHNCYRDTLIVTCTNSATSTFAGFVIFSGFMAN-- 531
 QY 363 NEKCVNAEAKILGYLNTNVLSDRLIPPHVNFSLHTTKDYMEMDNVIMTKEDQFSALGL 422
 DB 532 ERKVNIEV----- 540
 QY 423 DPCLEDELKSVQGTGLAFIAFTAMTHPTSPFWSVFFLMLINLGLSGMIGT 482
 DB 541 -----ADQGPGLAFVYVPEALTRPLSPFWAIIFFLMLLTGLDTHFATETIV 589

QY 483 TPIIDT-----SKVPKEMFTVGCCVFTFLVGLLEFVQVSGNRYFVTFMDDYSATLPLTLVIL 538
 DB 590 TSISDEFKPYLTHRPVFTLGGCICFCIFMGPMITGGIYMFQVLDVTAASAYALVIAIF 649
 QY 539 ENIAVAWIYGPKKMOELTEMLGFRPYRYFYVMKVFSPCLMAVLITASIIOLGVTTPAY 598
 DB 650 ELVGISYVGLQRFCEDEIMMIGFQPNIFWKVCWAEVTPILTILFCFSYQW--EPMTY 707
 QY 599 SAWIKKEAAERYLYFPNPMALLITLIVVATLPIPVVFLRHLPHLLSDGNTLSVSYKKA 658
 DB 708 GSY-----RY-----PNWSMVLGWLMLACSVIWIPIWIKMY--LAPG----- 744
 QY 659 RMMKDISNLEENDETRFILSKYVSEAPSPMPHRSRILGPGSTSPLETS 706
 DB 745 RFI-----ERLKLVCSPQPDNGPF-LAQRHGRERYKNMIDPLGTS 782
 RESULT 11
 US-09-191-468-120
 ; Sequence 120, Application US/09191468A
 ; Patent No. 6416375
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallagher, Michael J.
 ; APPLICANT: Burgess, Loyd R.
 ; APPLICANT: Brunden, Kurt R.
 ; TITLE OF INVENTION: Human Glycine Transporter Type 2
 ; FILE REFERENCE: 12311US01
 ; CURRENT APPLICATION NUMBER: US/09/191,468A
 ; CURRENT FILING DATE: 1998-11-12
 ; NUMBER OF SEQ ID NOS: 124
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 120
 ; LENGTH: 797
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-191-468-120

Query Match 26.9%; Score 1025.5; DB 4; Length 797;
 Best Local Similarity 33.6%; Pred. No. 4.1e-92;
 Matches 220; Conservative 110; Mismatches 191; Indels 133; Gaps 12;
 QY 36 SVLNVAGAGKQKAVEEELDAED--RPAWNSKLOYILAOIGFSGVLGNWFFPFLCOKN 93
 DB 173 SVATVATQ-----EDEQGDGKARGNWSKLDLILSMVGAVGLGNWVRFPYLAFO 224
 QY 94 GGGAYLVPLVLLIIIGIPLFLEAVGQRIIRGSGIGVWHYICPRLGGIGFSSCIVCLFV 153
 DB 225 GGGAYLVPLVLLIIIGIPLFLEAVGQRIIRGSGIGVWHYICPRLGGIGFSSCIVCLFV 153
 QY 154 GLYNNVIIGWSIFYFFKFSQYPLPWSEC----- 181
 DB 284 AIYNNVIICYTLFYLASFVSFLPWGSCNNPNTPECKDKTKLLDSCVISDHPKIQIKN 343
 QY 182 -----PVRNCSVAVVAEAECKSSATTYFWYREALDISDSISESGLANWMTLCLLV 233
 DB 344 STFCMTAYPNVNTMNTSLANKTFVSGSEEFKY-FVLKISAGIEYPCGIRWPLPFCLFL 402
 QY 234 WSTGGMAVGVGIOSGKVMYFSSLPYVVLACFLVRLGALLRGAVDGIHMTPTKLVKML 293
 DB 403 AWIIVYASLAKIGTSGKVIYFTATFPYVVLVILLIRGVTLPAGAGIWIYFITPKWEKLT 462
 QY 294 DPQVWREVAQVFFGLGFGGVIVFSSYNKQDNCHFDGALVSEINFSTVSLATLVFV 353
 DB 463 DATVWKAATQIFPFLSAAGWGLLTLSSYNKFNHNCYRDTLIVTCTNSATSTFAGFVIFS 522
 QY 354 VLGFKANIMNCKVVENAEKILGYLNTNVLSDRLIPPHVNFSLHTTKDYMEMDNVIMTKV 413
 DB 523 VIGFMAN--ERKVNIEV----- 538
 QY 414 EDQFSALGLDPCLEDELKSVQGTGLAFIAFTAMTHPTSPFWSVFFLMLINLGLSG 473
 DB 539 -----ADQGPGLAFVYVPEALTRPLSPFWAIIFFLMLLTGLDTHFATETIV 578

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 638 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-240-783B-2

Query Match 26.3%; Score 1003; DB 1; Length 638;
Best Local Similarity 31.3%; Pred. No. 4.8e-90;
Matches 224; Conservative 132; Mismatches 224; Indels 136; Gaps 16;

QY 40 VAGEAGKQKAVEEELDAED----RPAWNSKLYLAQIGFSGVLGNIRWPPYLCQKNG 95
Db 8 VATSSPEQNGAVPSEATKDONLTRGNWNGQIEFVLTSGVAVGLGNWVRPPYLCYRNG 67

QY 96 GAYLVPLVLLIIGIPFLFELEAVGQIRRGSTGVVHICPRGGIGFSSCIYCLFVGL 155
Db 68 GAFMFPYFIMLVFCGIPFLFMEISFGQFASQCGCLGVNR-ISPMPKGVGYMMVYSTYIGI 126

QY 156 YVNVIIIGWSIFYFKFOYPLPWSEC-----PVRNGSVA-V 191
Db 127 YVNVICIAFYFESSMTHVLPWAYCNPWNTPCAGVLDASNLNGSRPTALSLSHL 186

QY 192 VEAECKSSATTYFWREALDISISSEGLNKKMTLCLLVWSIGMAVKGQSSGK 251
Db 187 FNVTLQRTSPSEEWRLYVLKLSDDIGDFGEVRLPLLGLCGVSWVWVFLIRGVKSSGK 246

QY 252 VMFESSLPVYVLAFLVRLGALLRGAVDGLHMETPKLVKMLDPQVWREVATQVFFGL 311
Db 247 VVYFTATFPYVWLTILFVRGVTLEGAFTGIMYLTLPKWKILEAKWGDAAASQIFYSLGC 306

QY 312 GFGGVIVFSSYNKODNCHDFGALVSFINFTSVLATLVFVFLGFKANINNEKCVENA 371
Db 307 AWGLITMASYNKFNHNCYRDSVLIISITNCATSVAGFVIFSLGFMAN----- 355

QY 372 EKILGYLNTNVLSDRLIPPHVNFSLTKDYMEMDNVIMTVKEDQFSALGLDPCLEDEL 431
Db 356 -----HLGVDVSRVAD-- 366

QY 432 DKSVOGTGLAFIAFTTEAMTHPTSPFWSVMEFLMLINILGSMIGTMAGITPIIDTSKV 491
Db 367 -----HGPGAFVAYPEALTLLPISPLWSLLFFMLILGLGTQFCLETLTAIVD--EV 420

QY 492 PKEMF-----TVGCCVFTPLVGLLVQSRGNYFVMDFDYSATPLTLTILVILENIAVA 544
Db 421 GNEWILQKKYVTLGVAVAGELLLGIPLTSQAGIYWLMLMDNYAASFSLVISCIMCVSIM 480

QY 545 WIYGPKKFMOELTEMLGFRPYRYFYMMKFVSPICMAVLTASITQLGVTTPAYSANIKE 604
Db 481 YIYGHRYFQDIQMLGFPPLFFQICWRVFSPTIIFILIFTVIQ--YRPTIYN----- 533

QY 605 EAAERYLYFPNPMAL--LITLIVATLPIPVFVLRHFLHLLSDGNTLSVYKKARMK 662
Db 534 -----HYQYPGWAIVAIGLMAISVICIPLALFQL-----CRTGDDTLQLRKNATKPSR 584

QY 663 DIS-NLENDRETLRSKVSAPSP-----MPTHRS-----YLGPGSTSPLETS 706
Db 585 DWGPALEHRTGRI-----APTITSPEDGFEVQPLHPDKAIPVIGSNGSSRLQDS 636

RESULT 14
US-09-084-813-2
; Sequence 2, Application US/09084813
; Patent No. 6127131
; GENERAL INFORMATION:
; APPLICANT: Smith, Kelli
; APPLICANT: Borden, Laurence A.
; APPLICANT: Branchet, Theresa
; APPLICANT: Hartig, Paul R.
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A GLYCINE TRANSPORTER AND USES
; TITLE OF INVENTION: THEREOF

; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/084,813
; FILING DATE: 26-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1795/39875-AZ-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 638 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-084-813-2

Query Match 26.3%; Score 1003; DB 3; Length 638;
Best Local Similarity 31.3%; Pred. No. 4.8e-90;
Matches 224; Conservative 132; Mismatches 224; Indels 136; Gaps 16;

QY 40 VAGEAGKQKAVEEELDAED----RPAWNSKLYLAQIGFSGVLGNIRWPPYLCQKNG 95
Db 8 VATSSPEQNGAVPSEATKDONLTRGNWNGQIEFVLTSGVAVGLGNWVRPPYLCYRNG 67

QY 96 GAYLVPLVLLIIGIPFLFELEAVGQIRRGSTGVVHICPRGGIGFSSCIYCLFVGL 155
Db 68 GAFMFPYFIMLVFCGIPFLFMEISFGQFASQCGCLGVNR-ISPMPKGVGYMMVYSTYIGI 126

QY 156 YVNVIIIGWSIFYFKFOYPLPWSEC-----PVRNGSVA-V 191
Db 127 YVNVICIAFYFESSMTHVLPWAYCNPWNTPCAGVLDASNLNGSRPTALSLSHL 186

QY 192 VEAECKSSATTYFWREALDISISSEGLNKKMTLCLLVWSIGMAVKGQSSGK 251
Db 187 FNVTLQRTSPSEEWRLYVLKLSDDIGDFGEVRLPLLGLCGVSWVWVFLIRGVKSSGK 246

QY 252 VMFESSLPVYVLAFLVRLGALLRGAVDGLHMETPKLVKMLDPQVWREVATQVFFGL 311
Db 247 VVYFTATFPYVWLTILFVRGVTLEGAFTGIMYLTLPKWKILEAKWGDAAASQIFYSLGC 306

QY 312 GFGGVIVFSSYNKODNCHDFGALVSFINFTSVLATLVFVFLGFKANINNEKCVENA 371
Db 307 AWGLITMASYNKFNHNCYRDSVLIISITNCATSVAGFVIFSLGFMAN----- 355

QY 372 EKILGYLNTNVLSDRLIPPHVNFSLTKDYMEMDNVIMTVKEDQFSALGLDPCLEDEL 431
Db 356 -----HLGVDVSRVAD-- 366

QY 432 DKSVOGTGLAFIAFTTEAMTHPTSPFWSVMEFLMLINILGSMIGTMAGITPIIDTSKV 491
Db 367 -----HGPGAFVAYPEALTLLPISPLWSLLFFMLILGLGTQFCLETLTAIVD--EV 420

QY 492 PKEMF-----TVGCCVFTPLVGLLVQSRGNYFVMDFDYSATPLTLTILVILENIAVA 544
Db 421 GNEWILQKKYVTLGVAVAGELLLGIPLTSQAGIYWLMLMDNYAASFSLVISCIMCVSIM 480

QY 545 WIYGPKKFMOELTEMLGFRPYRYFYMMKFVSPICMAVLTASITQLGVTTPAYSANIKE 604
Db 481 YIYGHRYFQDIQMLGFPPLFFQICWRVFSPTIIFILIFTVIQ--YRPTIYN----- 604

Db 481 YIYGRNYFQDIQMLGFPPLFFQICWRFVSPTIIFILFTVIQ--YRPITYN----- 533
QY 605 EAAERYLYFPNPMAL--LITLIVVATLPVPVFLRHFHLLSDGNTLSVSYYKARMK 662
Db 534 -----HYQYPCWAVAIGFLMALSSVICIPLIALFOL-----CRTDGDTLQRLKNAKPSR 584
QY 663 DIS-NLEENDETRFILSKVPSEAPSP-----MPTHRS-----YLGPGSTSPLETS 706
Db 585 DWGPALLEHRTGRY---APTTPSPEDGFEVQPLHPDKAQIPIVGNSGSSRLQDS 636

RESULT 15

US-09-343-361-13
; Sequence 13, Application US/09343361
; Patent No. 6225115

GENERAL INFORMATION:

; APPLICANT: Smith, Kelli E. et al
; TITLE OF INVENTION: DNA Encoding Taurine and GABA Transporters and Uses
; FILE REFERENCE: 40558-D
; CURRENT APPLICATION NUMBER: US/09/343,361
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 13
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-343-361-13

Query Match 26.3%; Score 1003; DB 4; Length 638;
Best Local Similarity 31.3%; Pred. No. 4.8e-90;
Matches 224; Conservative 132; Mismatches 224; Indels 136; Gaps 16;

QY 40 VAGEAGKQKAVREDAED---RPAWNSKLOYILAOIGFSGVLGNIRFPYLCOKNGS 95
Db 8 VATSSPQNGAVPSEATKQDNLTGRNGNQGIEFVLTSGVAVGLGNVWRFPYLCYRNGG 67
QY 96 GAYLVPLVLLIIIGIPLFFLELAVGQIRKRGSGVHYICPRLGGIGFSSCIVCLFVGL 155
Db 68 GAEMFPYFIMLVFCGIPLFFMELSGQFASQGLGVR-ISPMEKGVGYGMVVSITYGI 126
QY 156 YNVVIQWSIFYPFKSQYPLPWSEC-----PVRNGSVA-V 191
Db 127 YNVVVICIAFYFFSSMTHVLPWAYCNPWPNTPCAGVLDASNLNTNGSRPTALSGNLSH 186
QY 192 VEAECEKSSATTFWYREALDISISESGGLNWKMTLCLLVWSIGGMVAGKGIQSSGK 251
Db 187 FNYTLQRTSPSEYWRLYLVKLSDDIGDFGEVRLPLGLGLGVSWVVFCLIRGVKSSGK 246
QY 252 VMYFSSLPYVVLACFLVRGLLLRGAVDGIILHMFPPKLVKMLDPQVWRREVATQVFFGLGL 311
Db 247 VVYFATFPYVWLTLFVRGVTLLEGAFGIMVYLPKWKDILEAKVWGDAASQIFYSLGC 306
QY 312 GFGGVIVFSSYNKQDNCHDFGALVSFNFTSVLATLVVFLVGFKANIMNEKCVVNA 371
Db 307 AWGLITMASYNKFNHNCYRDSVITNCATSVYAGVIFVSIILGFMAN----- 355
QY 372 EKILGYLNTNVLSRDLIPPHVNFSHLTTKDYMEMDNVMTVKEDQFSALGLDPCLEDEL 431
Db 356 -----HLGVDVSRVAD-- 366
QY 432 DKSVOGTGLAFIATEAMTHPTSPFWSVMPFLMLINILGSMIGTMAGITTPIDTSKV 491
Db 367 ---HGPGLAFAVAYPEALTLLPISPLWSLLFFMLILLGLGTQFCLETLVTAIVD--EV 420
QY 492 PKEMF-----TVGCCVFTFLVGLLFVQRSGNYFTVTFDDYSATLPLTLVILENIAVA 544
Db 421 GNEWILQKTKYTVTLGVAVAGELLGPILTSSQAGIYVLLMDNVAASFSVLVVICMVSIM 480
QY 545 WIYGPKKFMQELTEMLGFRPVRFYFMKVFSPICMAVLTTTASIIQLGVTTPPAYSAWIK 604

Search completed: April 21, 2003, 13:59:16
Job time : 34 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 13:46:37 ; Search time 40 seconds
(without alignments)
2421.830 Million cell updates/sec

Title: US-09-923-444A-2

Perfect score: 3817

Sequence: 1 MPKNKVTQREHSSEHVETES.....NPNPGYGRGYLLASTPESEL 727

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23:	/SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3810	99.8	727	17	Human neurotransmi
2	3681	96.4	727	23	Human HIPHUM 00000
3	2522.5	66.1	730	22	Amino acid sequenc
4	2522.5	66.1	730	22	Human NNT7 protein
5	2522.5	66.1	730	23	Human GABA transpo
6	2522.5	66.1	730	23	Human neurotransmi
7	2483	65.1	729	23	Protein sequence i
8	1495.5	39.2	675	22	Drosophila melanog
9	1495.5	39.2	744	22	Drosophila melanog
10	1323	34.7	616	22	Human nerve mass-t

11	1318	34.5	647	20	AAW3376	Human HPDV78 prot
12	1307.5	34.3	592	23	AAE14408	Human neurotransmi
13	1307.5	34.3	634	23	AAE13282	Human transporters
14	1305	34.2	662	22	ABB59777	Drosophila melanog
15	1302.5	34.1	616	17	AAW07635	Rat brain derived
16	1273	33.4	392	22	AAG64743	Human sodium neuro
17	1037.5	27.2	797	21	AAW56380	Human Glyt-2 trans
18	1037.5	27.2	797	21	AAW56380	Human glycine tran
19	1036.5	27.2	797	19	AAW56372	Amino acid sequenc
20	1036.5	27.2	797	19	AAW56373	Human Glyt-2 trans
21	1036.5	27.2	797	19	AAW56374	Human Glyt-2 trans
22	1036.5	27.2	797	19	AAW56376	Human Glyt-2 trans
23	1036.5	27.2	797	19	AAW56385	Human Glyt-2 trans
24	1036.5	27.2	797	21	AAW56368	Amino acid sequenc
25	1036.5	27.2	797	21	AAW09898	Human glycine tran
26	1036.5	27.2	797	21	AAW56380	Human glycine tran
27	1036.5	27.2	797	21	AAW56382	Human glycine tran
28	1036.5	27.2	797	21	AAW56382	Human glycine tran
29	1035.5	27.1	797	19	AAW56384	Human Glyt-2 trans
30	1035.5	27.1	797	19	AAW56384	Human Glyt-2 trans
31	1032.5	27.1	797	21	AAW56384	Human glycine tran
32	1032.5	27.1	797	21	AAW56384	Human glycine tran
33	1032.5	27.1	797	21	AAW56384	Human glycine tran
34	1031.5	27.0	797	19	AAW56377	Human Glyt-2 trans
35	1031.5	27.0	797	19	AAW56378	Human Glyt-2 trans
36	1031.5	27.0	797	19	AAW56369	Amino acid sequenc
37	1031.5	27.0	797	21	AAW82115	Human SC polypepti
38	1030.5	27.0	797	19	AAW56375	Human Glyt-2 trans
39	1030.5	27.0	797	19	AAW56383	Human Glyt-2 trans
40	1029.5	27.0	797	19	AAW56386	Human Glyt-2 trans
41	1029.5	27.0	797	21	AAW09897	Human glycine tran
42	1028.5	26.9	797	19	AAW56381	Human Glyt-2 trans
43	1025.5	26.9	797	19	AAW56379	Human Glyt-2 trans
44	1025.5	26.9	797	21	AAW09896	Human glycine tran
45	1025.5	26.9	797	21	AAW56382	Human glycine tran

ALIGNMENTS

RESULT 1
AAR88390
ID AAR88390 standard; Protein; 727 AA.
XX AAR88390;
XX AC
XX 15-OCT-1996 (first entry)
DT Human neurotransmitter transporter protein.
DE Neurotransmitter transporter protein; pain therapy; stroke therapy;
KW amyotrophic lateral sclerosis.
XX Homo sapiens.
XX WO9531539-A1.
XX 23-NOV-1995.
XX 16-MAY-1994; 94WO-US05363.
XX 16-MAY-1994; 94WO-US05363.
PR 26-MAY-1994; 94ZA-0003696.
PD 23-NOV-1995.
PF 16-MAY-1994; 94WO-US05363.
XX 16-MAY-1994; 94WO-US05363.
PR 26-MAY-1994; 94ZA-0003696.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Fleischmann RD, Li Y;
PI WPI; 1996-010925/01.
DR N-PSDB; AAT09866.
XX DNA encoding neuro:transmitter transporter protein and related
PT (ant)agonists - useful to treat e.g., amyotrophic lateral sclerosis,

PT pain and stroke.

PS Claim 1; Fig.1; 53pp; English.

CC This neurotransmitter transporter protein may be expressed recombinantly in a host microorganism using a vector plasmid.

CC NRT antagonists may be used to treat amyotrophic lateral sclerosis, pain and strokes. NRT antagonists/inhibitors may be used to treat neurological and psychiatric disorders, e.g. depression, anxiety and epilepsy.

XX SQ Sequence 727 AA;

Query Match 99.8%; Score 3810; DB 17; Length 727;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 726; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPKNSKVTOREHSHSVHTESVADLLALEPVDYKQSVLNVAGEAGGKQKAVEEELDAEDR 60
 Db 1 MPKNSKVTOREHSHSVHTESVADLLALEPVDYKQSVLNVAGEAGGKQKAVEEELDAEDR 60
 QY 61 PAWNSKLOYLIAQIGFSVGLGNWRFPYLCQKNGGAYLVPYLVLLIIIGIPFFLELAV 120
 Db 61 PAWNSKLOYLIAQIGFSVGLGNWRFPYLCQKNGGAYLVPYLVLLIIIGIPFFLELAV 120
 QY 121 GQIRIRGSGVWHYICPRLLGIGFSSCIYVCLFVGLYNNVIIGWSIFYFFKSFQYPLPWS 180
 Db 121 GQIRIRGSGVWHYICPRLLGIGFSSCIYVCLFVGLYNNVIIGWSIFYFFKSFQYPLPWS 180
 QY 181 CPVVRNGSVAVVEACEKSSATTYFWYREALDSDSISSEGLNWKMTCLLVVWSIGGM 240
 Db 181 CPVVRNGSVAVVEACEKSSATTYFWYREALDSDSISSEGLNWKMTCLLVVWSIGGM 240
 QY 241 AVKGIOSSGKVMYFSSLPFYVWLACFLVRLGALLRGAVDGLIHMTFPLKLVKMLDPQVWRE 300
 Db 241 AVKGIOSSGKVMYFSSLPFYVWLACFLVRLGALLRGAVDGLIHMTFPLKLVKMLDPQVWRE 300
 QY 301 VATQVFFGLGFGGVIVFSSYNKQDNCHFDGALVSFINFTSVLATLVVFFVLGFKAN 360
 Db 301 VATQVFFGLGFGGVIVFSSYNKQDNCHFDGALVSFINFTSVLATLVVFFVLGFKAN 360
 QY 361 IMNEKCVVENAEKILGYLNTNVLSDLPHPVNFSLTTKDYMEMDNVIMTKEDQFSAL 420
 Db 361 IMNEKCVVENAEKILGYLNTNVLSDLPHPVNFSLTTKDYMEMDNVIMTKEDQFSAL 420
 QY 421 GLDPCLEDELKSVQGTGLAFIAFTEAMTHPTSPFWSVFFLMLINLGLSGMIGTMAG 480
 Db 421 GLDPCLEDELKSVQGTGLAFIAFTEAMTHPTSPFWSVFFLMLINLGLSGMIGTMAG 480
 QY 481 ITTPTIDTSKVPKEMFTVCCVFTFLVGLLFFVQSGNRYFTVTFDDYSATLPLTLVILEN 540
 Db 481 ITTPTIDTSKVPKEMFTVCCVFTFLVGLLFFVQSGNRYFTVTFDDYSATLPLTLVILEN 540
 QY 541 IAVMIYGPKFMQBELTMLGPRPYRFYFMKVFSPICMAVLTTASIIQLGVTPPAYSA 600
 Db 541 IAVMIYGPKFMQBELTMLGPRPYRFYFMKVFSPICMAVLTTASIIQLGVTPPAYSA 600
 QY 601 WKEEAAERYLYFPNPMALLITLIVATLPIPVVFLRHFHLLSDGNTLSVSYKKARM 660
 Db 601 WKEEAAERYLYFPNPMALLITLIVATLPIPVVFLRHFHLLSDGNTLSVSYKKARM 660
 QY 661 MKDISLNEENDETRILSKVSEAPSPMPTHRSYLPGGSTPLETSWNPNPGYGRGYLLA 720
 Db 661 MKDISLNEENDETRILSKVSEAPSPMPTHRSYLPGGSTPLETSWNPNPGYGRGYLLA 720
 QY 721 STPESEL 727
 Db 721 STPESEL 727

RESULT 2

AAE21800

*ID AAE21800 standard; Protein; 727 AA.

XX

AC AAE21800;

DT 16-JUL-2002 (first entry)

DE Human HIPHUM 0000029 protein.

XX Human; neurotransmitter transporter polypeptide; HIPHUM 0000029 protein;
 XX prophylaxis; psychiatric disorder; bipolar disorder; psychotic disorder;
 XX unipolar depression; anxiety; schizophrenia; neurodegenerative disorder;
 XX neurological disorder; drug dependence; gene therapy; chromosome 1p21.

OS Homo sapiens.

XX GB2365432-A.

XX 20-FEB-2002.

XX 19-MAY-2000; 2000GB-0012199.

XX 19-MAY-2000; 2000GB-0012199.

XX (GLAX) GLAXO GROUP LTD.

XX Sala CF, Terstappen GC;

XX WPI; 2002-317841/36.

XX N-PSDB; AAD34007.

XX An isolated neurotransmitter transporter polypeptide HIPHUM 0000029,
 XX whose regulation is useful in treating or preventing disease such as
 XX anxiety or depression -

XX Claim 1; Page 25-28; 39pp; English.

XX The invention relates to human neurotransmitter transporter polypeptides
 CC referred to as HIPHUM 0000029 and nucleic acid molecules encoding such
 CC polypeptides. Sequences of the invention their agonists and antagonists
 CC are useful for preparing a medicament for treatment or prophylaxis of
 CC disorders such as psychiatric disorders, bipolar disorders, unipolar
 CC depression, anxiety, schizophrenia, psychotic disorders, neurological/
 CC neurodegenerative disorders and drug dependence. Polynucleotides of the
 CC invention are useful as primers and probes. They are also used in gene
 CC therapy. The present sequence is human HIPHUM 0000029 protein. The
 CC HIPHUM 0000029 gene is located on chromosome 1p21.

XX SQ Sequence 727 AA;

Query Match 96.4%; Score 3681; DB 23; Length 727;

Best Local Similarity 97.0%; Pred. No. 0;

Matches 705; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 1 MPKNSKVTOREHSHSVHTESVADLLALEPVDYKQSVLNVAGEAGGKQKAVEEELDAEDR 60

Db 1 MPKNSKVTOREHSHSVHTESVADLLALEPVDYKQSVLNVAGEAGGKQKAVEEELDAEDR 60

QY 61 PAWNSKLOYLIAQIGFSVGLGNWRFPYLCQKNGGAYLVPYLVLLIIIGIPFFLELAV 120

Db 61 PAWNSKLOYLIAQIGFSVGLGNWRFPYLCQKNGGAYLVPYLVLLIIIGIPFFLELAV 120

QY 121 GQIRIRGSGVWHYICPRLLGIGFSSCIYVCLFVGLYNNVIIGWSIFYFFKSFQYPLPWS 180

Db 121 GQIRIRGSGVWHYICPRLLGIGFSSCIYVCLFVGLYNNVIIGWSIFYFFKSFQYPLPWS 180

QY 181 CPVVRNGSVAVVEACEKSSATTYFWYREALDSDSISSEGLNWKMTCLLVVWSIGGM 240

Db 181 CPVVRNGSVAVVEACEKSSATTYFWYREALDSDSISSEGLNWKMTCLLVVWSIGGM 240

QY 241 AVKGIOSSGKVMYFSSLPFYVWLACFLVRLGALLRGAVDGLIHMTFPLKLVKMLDPQVWRE 300

Db 241 AVKGIOSSGKVMYFSSLPFYVWLACFLVRLGALLRGAVDGLIHMTFPLKLVKMLDPQVWRE 300

QY 301 VATQVFFGLGFGGVIVFSSYNKQDNCHFDGALVSFINFTSVLATLVVFFVLGFKAN 360


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Db 59 DERPAWNSKLOYLLAQVGSVGNWRRPYLCQKNGGGAYLLPYLLMLVIGIPLEFLE 118
Qy 118 LAVGQIRRGSGVWHYICPRIGGIFSSCIVCLFVGLYNNVIGWISFYFFKFSQYPLP 177
Db 119 LSVGQIRRGSGVWNYISPKLGGIFASCVYFVALYNNVIGWISFYFFKFSQYPLP 178
Qy 178 WSECPVVRNGSVAVVAEAEKSSATTYFYWREALDISDSISSEGLNWKMTCLLVVWSI 237
Db 179 WDQCPLVKNASHTFVEPECEQSSATTYFYWREALNISSESGLNWKMTICLLAAWVM 238
Qy 238 GGMVAGKGIQSSGKVMYFSSLPYVVLACFLVRGLLRGAVDGIHMFYFKLVKMLDPQV 297
Db 239 VCLAMIKGIQSSGKIIFSSLPYVVLICFLIRAFLLNGSIDGIRHMFYFKLVKMLDPQV 298
Qy 298 WREAVATQVFFGLGFGGVIVFSSYNKQDNCHFGALVSFINFTSVLATLVVAVLGF 357
Db 299 WREAVATQVFFGLGFGGVIVFSSYNKQDNCHFGALVSFINFTSVLATLVVAVLGF 358
Qy 358 KANIMNEKCVVENAEKILGYLNTNVLSDRLIPPHVNFSLTTRKDYMEMDNVIMTKEDQF 417
Db 359 KANVINEKICITONSETIMKFLKMGNISQDILPHHINLSTVTAEDYHLVYDIQKVEEF 418
Qy 418 SALGLDPCILLELDSKSVQGTGLAFIAFTEAMTHFTSPFWSVMMFLMLNLGLSGMGT 477
Db 419 PALHNSCKIEEELNKAVOGTGLAFIAFTEAMTHFTSPFWSVMMFLMLNLGLSGMGT 478
Qy 478 MAGITTPITIDTSKVPKEMFTVGCCTFLVGLLVQVRSNGYFVTMFDYDYSATLPLTLVI 537
Db 479 IEGIVTPIVDTFKVRKEILTVCICLLAFCLGLIFVQVRSNGYFVTMFDYDYSATLPLTLVI 538
Qy 538 LENIAVAVIYIGPKPKMOELTEMLGFRPYFYFMKVFVSPCLMAVLTASIIQLGVTPPA 597
Db 539 LENIAVCFVYIDKFMEDLMDLGFAPSYFYFYMMYKISPLMLLSLLIASVWNNGLSPG 598
Qy 598 YSAWIKKEAERYLYFPNPMALLITLIVATLPIPVFVLRHFLHLLSDGS-NTLSVSYK 656
Db 599 YNAWIEDKASEEFLSYPTWGLVVCVSLVFAILPVFVLRHFLHLLSDGS-NTLSVSYK 658
Qy 657 KARMKIDISLENDETRILSKVPSEAPSPMPTHRSLYGLPGSTSPSTSWNPNPGYGRG 716
Db 659 RGRVLKEPVNL-EGDDTSLIHGKIPSEMPSPNFKNRYKQSGSPTLDTA--PNGRYGIG 715
Qy 717 YLLA---STPESEL 727
Db 716 YLMADIMPDPESDL 730

RESULT 4
AA72908
ID AA72908 standard; Protein; 730 AA.
AC AA72908;
XX
XX
XX 13-JUN-2001 (first entry)
XX
XX Human NTT7 protein.
XX
XX Human; NTT7 protein; psychiatric disorder; anxiety; depression;
XX schizophrenia; phobia; panic disorder; obsessive compulsive disorder;
XX Parkinson's disease; central nervous system disorder; cerebroprotective;
XX neurological disorder; stroke; pain; neuropathic pain; sleep disorder;
XX tranquilizer; analgesic; neuroleptic; vaccine.
XX
XX Homo sapiens.
XX
XX WO200119854-A2.
XX
XX 22-MAR-2001.
XX
XX 14-SEP-2000; 2000WO-GB03541.
XX
XX 15-SEP-1999; 99GB-0021833.
XX
XX
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PR 17-MAR-2000; 2000GB-0006545.
XX (SMIK ) SMITHLINE BEECHAM PLC.
XX Hill J, Duckworth DM, Farmer M, Pangalos M;
XX WPI; 2001-244780/25.
DR N-PSDB; AAD03039.
XX
XX Novel NTT7 polypeptide useful for treating anxiety, depression,
XX schizophrenia, phobia, Parkinson's disease, stroke, pain, and
XX psychiatric, panic, neurological, central nervous system, obsessive
XX compulsive and sleep disorders.
XX
XX Claim 3; Page 20; 27pp; English.
XX
XX The present sequence is human NTT7 protein encoded by a cDNA. NTT7 is
XX thought to be a member of the neurotransmitter family of polypeptides.
XX NTT7 sequences are useful for treating psychiatric disorders, anxiety,
XX depression, schizophrenia, phobias, panic disorder, obsessive compulsive
XX disorder, Parkinson's disease, central nervous system disorders, stroke,
XX neurological disorders, pain, neuropathic pain, sleep disorders, and
XX diseases in which neurotransmitters are implicated. NTT7 sequences are
XX useful for screening antagonists and agonists of NTT7 and as vaccines
XX for inducing immunological response in a mammal. NTT7 sequences and its
XX antibodies are useful to configure screening methods for detecting the
XX effect of added compounds on the production of mRNA and polypeptide in
XX cells. NTT7 is useful in conventional low capacity screening methods and
XX also in high-throughput screening (HTS) formats and is useful for
XX identifying membrane bound or soluble receptors. NTT7 antibody is useful
XX to isolate or identify clones expressing NTT7 or to purify NTT7 by
XX affinity chromatography. NTT7 is useful as diagnostic reagent for
XX detecting mutations in the associated gene, and for chromosome
XX localisation studies and tissue expression studies.
XX
XX Sequence 730 AA;
```

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Query Match 66.1%; Score 2522.5; DB 22; Length 730;
Best Local Similarity 64.4%; Pred. No. 6.3e-250;
Matches 473; Conservative 114; Mismatches 135; Indels 13; Gaps 8;
```

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Qy 1 MPKNSKYVQREHSHVTSVADLLALEPVD--YKQSVLNVAGEAGGKOKAVEEELDAE 58
Db 1 MPKNSKYVQRE--LDDVTSVADLLSNEADDAADAKTSELIVDQGE-EXKDTDEGESE 58
Qy 59 D-REPAWNSKLOYLLAQIGFSVGLGNWRFPYLCQKNGGGAYLLPYLLMLVIGIPLEFLE 117
Db 59 D-REPAWNSKLOYLLAQIGFSVGLGNWRFPYLCQKNGGGAYLLPYLLMLVIGIPLEFLE 118
Qy 118 LAVGQIRRGSGVWHYICPRIGGIFSSCIVCLFVGLYNNVIGWISFYFFKFSQYPLP 177
Db 119 LSVGQIRRGSGVWNYISPKLGGIFASCVYFVALYNNVIGWISFYFFKFSQYPLP 178
Qy 178 WSECPVVRNGSVAVVAEAEKSSATTYFYWREALDISDSISSEGLNWKMTCLLVVWSI 237
Db 179 WDQCPLVKNASHTFVEPECEQSSATTYFYWREALNISSESGLNWKMTICLLAAWVM 238
Qy 238 GGMVAGKGIQSSGKVMYFSSLPYVVLACFLVRGLLRGAVDGIHMFYFKLVKMLDPQV 297
Db 239 VCLAMIKGIQSSGKIIFSSLPYVVLICFLIRAFLLNGSIDGIRHMFYFKLVKMLDPQV 298
Qy 298 WREAVATQVFFGLGFGGVIVFSSYNKQDNCHFGALVSFINFTSVLATLVVAVLGF 357
Db 299 WREAVATQVFFGLGFGGVIVFSSYNKQDNCHFGALVSFINFTSVLATLVVAVLGF 358
Qy 358 KANIMNEKCVVENAEKILGYLNTNVLSDRLIPPHVNFSLTTRKDYMEMDNVIMTKEDQF 417
Db 359 KANVINEKICITONSETIMKFLKMGNISQDILPHHINLSTVTAEDYHLVYDIQKVEEF 418
Qy 418 SALGLDPCILLELDSKSVQGTGLAFIAFTEAMTHFTSPFWSVMMFLMLNLGLSGMGT 477
Db 419 PALHNSCKIEEELNKAVOGTGLAFIAFTEAMTHFTSPFWSVMMFLMLNLGLSGMGT 478
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QY 478 MAGITTPIDTSKVPKEMFTYGCCTFVLGLLFVORSGNRYFTVTFDDYSATLPLTLIVI 537
Db 479 IEGIVTPIVDFKVRKEILTVCCLLAEICGLIFVORSGNRYFTVTFDDYSATLPLTLIVI 538
QY 538 LENIAVMIYGPKKFQMDELTEMLGFRPYRFFYMMKFVSPCLMAVLTTASIIQLGVTPPA 597
Db 539 LENIAVCFVYGDIDKFMEDKMDLGFAPSRYYVMKYSPLMLLSLLIASVVMGLSPPG 598
QY 598 YSAWIKKEAARYLYFFPNWPMALLITLIVATLPVVFVLRHFHLLSDGS--NTLSVSYK 656
Db 599 YNAWIEDKASEEFLSYPTWGLVVCVULVFAILPVPVFIIVRRFNLIIDDSSGNLASVTYK 658
QY 657 KARMKDINSLEENDETFFILSKVSEAPSPMPTHRSLVPGCSTSPLETSMNPNPGYGRG 716
Db 659 RGRVLKEPVNL-EGDTSLSHGKIPSEMPSPNFGRIYKQSGSTLDTA--PNGRYGIG 715
QY 717 YLLA----STPESEL 727
Db 716 YLMADIMPDMPESDL 730

RESULT 5
ABB77168
ID ABB77168 standard; Protein; 730 AA.
XX
AC ABB77168;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human GABA transporter protein.
XX
KW Human; GABA; transporter protein; drug screening; therapeutic target.
XX
OS Homo sapiens.
XX
FH Key
FT Region
FT 19..21 Location/Qualifiers
FT /label= Protein_kinase_C_phosphorylation_site
FT 19..22
FT /label= Casein_kinase_II_phosphorylation_site
FT 25..28
FT /label= Casein_kinase_II_phosphorylation_site
FT 49..52
FT /label= Casein_kinase_II_phosphorylation_site
FT 55..58
FT /label= Casein_kinase_II_phosphorylation_site
FT 85..99
FT /label= Sodium:neurotransmitter_symporter_family_
FT 126..129 signature_1
FT /label= cAMP- and cGMP-dependant_protein_kinase_
FT 137..139 phosphorylation_site
FT /label= Protein_kinase_C_phosphorylation_site
FT 142..147
FT /note= "Gly is N-myristoylated"
FT 187..190
FT /note= "Asn is N-glycosylated"
FT 191..194
FT /label= Casein_kinase_II_phosphorylation_site
FT 213..216
FT /note= "Asn is N-glycosylated"
FT 217..220
FT /label= Casein_kinase_II_phosphorylation_site
FT 246..251
FT /note= "Gly is N-myristoylated"
FT 250..252
FT /label= Protein_kinase_C_phosphorylation_site
FT 276..279
FT /note= "Asn is N-glycosylated"
FT 277..282
FT /note= "Gly is N-myristoylated"
FT 287..289

/label= Protein_kinase_C_phosphorylation_site
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315..320
/note= "Gly is N-myristoylated"
383..386
/note= "Asn is N-glycosylated"
394..397
/note= "Asn is N-glycosylated"
399..402
/note= "Asn is N-glycosylated"
425..427
/note= "Asn is N-glycosylated"
438..443
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473..478
/note= "Gly is N-myristoylated"
477..482
/note= "Gly is N-myristoylated"
489..491
/note= "Gly is N-myristoylated"
522..525
/note= "Gly is N-myristoylated"
606..614
/note= "Gly is N-myristoylated"
618..623
/note= "Gly is N-myristoylated"
650..655
/note= "Gly is N-myristoylated"
656..658
/note= "Gly is N-myristoylated"
696..699
/note= "Gly is N-myristoylated"
/label= cAMP- and cGMP-dependant_protein_kinase_
phosphorylation_site

US2002031800-A1.
14-MAR-2002.
21-DEC-2000; 2000US-0741149.
05-SEP-2000; 2000US-229529P.
(LIZZ/) LI Z.
(CHAT/) CHATURVEDI K.
(ZHUS/) ZHU S.
(WOOD/) WOODAGE T.
(WEBB/) WEBSTER K.
(WEBB/) WEBSTER M.
(DFRA/) DI FRANCESCO V.
(BEAS/) BEASLEY E M.
Li Z, Chaturvedi K, Zhu S, Woodage T, Guegler K, Webster M;
Di Francesco V, Beasley EM;
WPI; 2002-361179/39.
N-PSDB; ABL55856, ABL55857.
New peptides and nucleic acid sequences related to the GABA transporter
subfamily, useful in developing diagnostic compositions, as well as in
drug screening, particularly as models for the development of human
therapeutic targets -
Claim 1; Fig 2; 69pp; English.
The sequence represents a novel human transporter protein of the GABA
transporter subfamily. The invention relates to a novel isolated human
peptide of the GABA transporter subfamily. The peptide and nucleic acids
are useful in developing human therapeutics and diagnostic compositions.
These are also useful in drug screening, particularly as models for the
development of human therapeutic targets.
Sequence 730 AA;
```

Query Match 66.1%; Score 2522.5; DB 23; Length 730;
Best Local Similarity 64.4%; Pred. No. 6.3e-250;
Matches 473; Conservative 114; Mismatches 135; Indels 13; Gaps 8;

```
QY 1 MPKNSKVQREHSHSVHTSVADLLALEPVD--YKQSVLNVAGEAGGKOKAVEEEDAE 58
Db 1 MPKNSKVYKRE-LDDVDVTSKDLNEEDAADADAFATSELIVDQGE-EKDTDDVEEGSEVE 58
QY 59 D-RPAWNSKLQVILAQIGSFVGLGNWRFPYLCQKNGGAYLVPYLVLLIIIGIPLFLE 117
Db 59 DERPAWNSKLQVILAQVGSFVGLGNWRFPYLCQKNGGAYLPLPYLLIMVIGIPLFLE 118
QY 118 LAVGORIRRGSTGVNHYICPRLGGIGFSFCVCLVGLVYVNIIGWSIFYFFKFSQYPLP 177
Db 119 LSVGORIRRGSTGVNHYISPKLGGIGFASCVVCFYVALYVNIIGWSLEFVSQSQQPLP 178
QY 178 WSECPVVRNGSVAVVEAECEKSSATYFYWYREALDIDSSESGLNWKMTLCILLVWSI 237
Db 179 WDQCPLVKNASHTFVEPECEQSATYFYWYREALNIDSSSESGLNWKMTICLLAAVWM 238
QY 238 GGMVAGKGIQSSGKVMYFSSLPYVVLACFLVRGLLLRGAVDGLIHMFTPKLVKMLDPQV 297
Db 239 VCLAMIKGIQSSGKIYFSSLPYVVLICFLIRAFLLNGSIDGIRHMTFKLEIMLEPKV 298
QY 298 WREAVATQVFFGLGGLGGVIVFSSYNKQDNCHDFDGVLSFINFTSVLATLVVVFVVLGF 357
Db 299 WREAVATQVFFGLGGLGGVIVFSSYNKQDNCHDFDGVLSFINFTSVLATLVVVFVVLGF 358
QY 358 KANTMNEKCVVENAEKILGLYNTNVLNRDLIPHVNFSLTTRDYMEMDNVMTVKEDQF 417
Db 359 KANVINEKCIQNSSETIMKFLKMGNSQDILPHHINLSVTAEYHLVDYDIIQKVKEEF 418
QY 418 SALGLDPCLEDELKSKVQGTGLAFIAFTFAMTHFTSPFWSVFFMLINLGLSGMIGT 477
Db 419 PALHNSCKIEBELKAVQGTGLAFIAFTFAMTHFTSPFWSVFFMLVNLGLSGMIGT 478
QY 478 MAGITPPIIDSKVPKEMFTVCCVFTFLVGLLFFVQSGNYFVTMFDYDYSATPLTLIVI 537
Db 479 IEGIVTPIVDTFKVRKEILTVCCLAFICGLIFVQSGNYFVTMFDYDYSATPLTLIWI 538
QY 538 LENTAVAVIYGPKEKMOELTFRPYRYFYVMKFSVPLCMVAVLTTASIIQIGVTPPA 597
Db 539 LENTAVCFVYGDKEKMEDKMLGAPSPRYFYVMKFSVPLCMVAVLTTASIIQIGVTPPA 598
QY 598 YSAWIKAEAEARYLYFPNPMALLITLIYVATLPIPVFVLRHFLHLSGDS-NTLSVSYK 656
Db 599 YNAWIEDKASEEFLSYPTWGLVVCVSLVVFVAILPVFVLRHFLHLSGDS-NTLSVSYK 658
QY 657 KARMKDISLENDDETFLSKVSEAPSPMTHRSYLGPGSTSPLETSWNPNGPYGRG 716
Db 659 RGRVLKEPVNL-EGDDTSLIHGKIPSEMPSPNFGKNYRKQSGSPTLDTA--PNGRYGIG 715
QY 717 YLLA----STPESEL 727
Db 716 YLMADIMPDPESDL 730
```

RESULT 6

AAEL14404

ID AAEL14404 standard; Protein; 730 AA.

XX AAEL14404;

AC AAEL14404;

DT 26-MAR-2002 (first entry)

XX Human neurotransmitter transporter, NTT-2.

XX Human; neurotransmitter transporter; NTT-2; transport disorder;
KW neurological disorder; psychiatric disorder; diabetes mellitus;
KW amyotrophic lateral sclerosis; Parkinson's disease; prostate cancer;
KW cardiac disorder; angina; Alzheimer's disease; amnesia; epilepsy;
KW sickle cell anaemia; stroke; Huntington's disease; psychiatric disorder;

KW acute stress disorder; anorexia nervosa; transgenic animal;
KW gene therapy; sodium:neurotransmitter symporter family; SNF.
XX Homo sapiens.
XX Location/Qualifiers
FH Domain
FT /label= Transmembrane_domain
FT 100..117
FT 335..359
FT /label= Transmembrane_domain
FT 460..483
FT /label= Transmembrane_domain
FT 494..512
FT /label= Transmembrane_domain
FT 572..589
FT /label= Transmembrane_domain
FT 619..640
FT /label= Transmembrane_domain
PN WO200190148-A2.
XX 29-NOV-2001.
XX 17-MAY-2001; 2001WO-US16283.
XX 19-MAY-2000; 2000US-205518P.
PR 22-JUN-2000; 2000US-213956P.
PR 28-JUN-2000; 2000US-215105P.
PR 14-JUL-2000; 2000US-218947P.
PR 27-JUL-2000; 2000US-228448P.
XX (INCY-) INCYTE GENOMICS INC.
XX Sanjanwala MS, Walia NK, Tribouley CM, Yue H, Gandhi AR, Ding L;
PI Yao MG, Lal P, Baughn MR, Hafalia A, Elliott VS, Patterson C;
PI Rankumar J;
XX WPI; 2002-097640/13.
DR N-PSDB; AAD23974.
XX Novel human neurotransmitter transporter polypeptides and
PT polynucleotides for diagnosing, preventing or treating transport,
PT neurological and psychiatric disorders and for identifying modulators
PT of therapeutic use
XX Claim 1; Page 111-113; 123pp; English.
PS The present sequence is human neurotransmitter transporter (NTT)-2
CC (Incyte ID No: 6881669CD1). The NTT-2 polypeptide contains
CC sodium:neurotransmitter symporter family (SNF) signature
CC sequences. The NTT polypeptide and polynucleotide
CC are useful for diagnosis, treatment and prevention of transport,
CC neurological and psychiatric disorders. Transport disorders
CC include akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia,
CC cystic fibrosis, Becker's muscular dystrophy, diabetes mellitus,
CC diabetes insipidus, myasthenia gravis, myocarditis, Parkinson's
CC disease, prostate cancer; cardiac disorders associated with transport
CC include angina, bradyarrhythmia, dermatomyositis, polymyositis;
CC neurological disorders associated with transport include Alzheimer's
CC disease, amnesia, bipolar disorder, dementia, depression, epilepsy,
CC Tourette's disorder, schizophrenia, and other disorders associated with
CC transport include neurofibromatosis, sickle cell anaemia, Wilson's
CC disease, cataracts, infertility, hyperglycaemia, hypoglycaemia, Graves'
CC disease, goitre, Cushing's disease, hypercholesterolaemia and
CC cystinuria. Neurological disorders treatable include epilepsy, stroke,
CC Huntington's disease, dementia and other extrapyramidal disorder,
CC motor neuron disorders, prion disease including kuru, metabolic disease
CC of the nervous system, and other developmental disorders of the central
CC nervous system, neuromuscular disorders, metabolic, endocrine and toxic
CC myopathies, periodic paralysis, mental disorders including mood and
CC anxiety. Psychiatric disorders include acute stress disorder, alcohol
CC dependence, anorexia nervosa, anxiety, obsessive-compulsive disorder,
CC panic disorder and sleep disorder. The polynucleotide is useful for

CC creating knockin humanised animals or transgenic animals to model
CC human disease and to detect and quantify gene expression in biopsied
CC tissues in which expression of NTR is correlated with disease. the
CC polynucleotide is also useful for generating hybridisation probes useful
CC in mapping the naturally occurring genomic sequence and oligonucleotide
CC primers derived from it are useful to detect single nucleotide
CC polymorphisms. NTR, its fragments and antibodies are useful as elements
CC on a microarray which is useful to monitor or measure protein-protein
CC interactions, drug-target interactions and gene expression profiles.
CC Sequences of the NTR polypeptide are used to analyse the proteome of a
CC tissue or cell type. The polypeptide of the invention is also useful for
CC screening its agonist, antagonist, modulator or a compound that binds
CC to it.

XX Sequence 730 AA;

Query Match 66.1%; Score 2522.5; DB 23; Length 730;
Best Local Similarity 64.4%; Pred. No. 6.3e-250;
Matches 473; Conservative 114; Mismatches 135; Indels 13; Gaps 8;

QY 1 MPKNSKVTRHSHSEHVTSVADLLALEPVD--YKQSVLNVAGEAGGKQKAVEEELDAE 58
Db 1 MPKNSKVKRE-LDDDVTSKDLDSNDAADAFKTSILVDGQE-EKDTDVEEGSEVE 58
QY 59 D-RPAWNSKLOYLQAIGFSVGLGNIRPPYLCQKNGGAYLVPYLVLIIGIPLFFLE 117
Db 59 DERPAWNSKLOYLQAIGFSVGLGNIRPPYLCQKNGGAYLVPYLVLIIGIPLFFLE 118
QY 118 LAVGQIRRGSTGVNHYICPRIGGGFSCICVCLFVGLYNNVIIGWSIFYFFKSFQYPLP 177
Db 119 LSVGQIRRGSTGVNHYISPKIGGIFASCVCYFVALYNNVIIGWSIFYFFKSFQYPLP 178
QY 178 WSECPVVRNGSVAVVAEACEKSSATTYFWYREALDISITSESGGLNWKMTCLCLLVVWSI 237
Db 179 WDCQFLVKNASHTFVEPECEQSATTYYWYREALNLSISSESGGLNWKMTCLCLLAQWV 238
QY 238 GOMAYGKGIQSSGKVMYFSSLPYVYVLAFLVGLLRLGAVDGIHMFTHPKLYKMLDPQV 297
Db 239 VCLAMIKGIQSSGKIYFSSLPYVYVLAFLVGLLRLGAVDGIHMFTHPKLYKMLDPQV 298
QY 298 WREAVATVFFGLGFGGVIVFSSYNKQDNCHDFCALVSFINFFTSVLAFLVFFVLGF 357
Db 299 WREAVATVFFGLGFGGVIVFSSYNKQDNCHDFDALVSFINFFTSVLAFLVFFVLGF 358
QY 358 KANIMNEKCVENAEKILGYLNTNLSRLDIPHPVNFSLHTTKDYEMDMNVMIVTKEDQF 417
Db 359 KANVINEKCIQNSSETIMFKLNGNISQDILPHINLSVTAEYHLVYDIIOKVKKEEF 418
QY 418 SALGLDPCLEDELKSVQGTGLAFTAFTEAMTHFTSPFWSYMFMLNLGLSGMIGT 477
Db 419 PALHNSCKIEBELNAVQGTGLAFTAFTEAMTHFTSPFWSYMFMLNLGLSGMIGT 478
QY 478 MAGIITPILDTSKVPKEMETVCCVTFVLVGLLFLVQSGNYFTVMDYDYSATPLTLIVI 537
Db 479 IEGIVTPVDTKVRKEILTITVCLLAFICGLIFVQSGNYFTVMDYDYSATPLTLIVI 538
QY 538 LENIAVAVTYGKPKMOELTMLGFRPYRYFYEMKFWFVSPCLMAVLTASTIOIGVTPPA 597
Db 539 LENIAVCFYVIGDKMEDLKMDFAPSYRYMYMYKWIISPLMLLSLLIASVVMNGLSPPG 598
QY 598 YSAWKEEAERYLPNPMALLITLIVATLPIPVFVLRHFLHLLSDGS-NTLSVSYK 656
Db 599 YNAWIEDKASEEFLSYPTWGLVVCVSLVFAILLPVVPVFTVRRFNLDDSSGNLASVYK 658
QY 657 KARMKMDISLNDENDETRIILSKVPSEAPSPMTHRSYLGPGTSPLSTSWNPNPGYGRG 716
Db 659 RGRVLKEPVNL-EGDDTSLIHGKIPSEMPSPNFGKIYRKQSGSPSLDTA--PNGRYGIG 715
QY 717 YLLA----STPESEL 727
Db 716 YLMADINPMPESDL 730

RESULT 7
AAO21215
ID AAO21215 standard; Protein; 729 AA.
XX
AC AAO21215;
DT 19-JUL-2002 (first entry)
XX
DE Protein sequence identified by SwissProt Accession No: Q08469.
XX
KW Antiparkinsonian; nootropic; neuroprotective; tranquiliser; vulneryary;
KW cerebroprotective; human sodium-dependent neurotransmitter transporter;
KW hybridising; central; peripheral nervous system disease; brain injury;
KW cerebrovascular disease; Parkinson's disease; corticobasal degeneration;
KW motor neuron disease; dementia; multiple sclerosis; post-stroke;
KW traumatic brain injury; stroke; post-traumatic brain injury;
KW small-vessel cerebrovascular disease; Alzheimer's disease; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200229048-A2.
XX
PD 11-APR-2002.
XX
PF 04-OCT-2001; 2001WO-EP11440.
XX
PR 05-OCT-2000; 2000US-237689P.
XX
PA (FARB) BAYER AG.
XX
PI Kohler RH;
XX
PS WPI; 2002-426112/45.
XX
PT New human sodium-dependent neurotransmitter transporter polypeptide,
PT the regulation of which is useful for treating central or peripheral
PT nervous system diseases e.g. brain injuries, Parkinson's disease, and
PT dementia
XX
PS Disclosure; Fig 3; 98pp; English.
XX
CC The invention relates to a purified human sodium-dependent
CC neurotransmitter transporter polypeptide comprising a sequence of 259
CC amino acids, given in the specification. A nucleic acid encoding the
CC protein is useful for detecting a polynucleotide encoding the protein in
CC a biological sample by hybridising the protein-encoding polynucleotide to
CC a nucleic acid material of a biological sample to form a hybridisation
CC complex, and detecting the hybridisation complex. The protein of the
CC invention and its encoding gene are useful for screening for agents which
CC decrease the activity of sodium-dependent neurotransmitter transporter
CC polypeptide by contacting the test compound with the protein or its gene
CC and detecting binding of the test compound to the protein or its gene. A
CC vector comprising the polynucleotide of the invention or a reagent that
CC modulates the activity of the protein or its gene is useful for the
CC preparation of a medicament for modulating the activity of sodium-
CC dependent neurotransmitter transporter in a disease. The reagent is
CC useful for treating diseases such as central or peripheral nervous system
CC disease, where the central nervous system disorders are selected from
CC brain injuries, cerebrovascular diseases and their consequences,
CC Parkinson's disease, corticobasal degeneration, motor neuron disease,
CC dementia, including multiple sclerosis, traumatic brain injury, stroke,
CC post-stroke, post-traumatic brain injury, small-vessel cerebrovascular
CC disease, and Alzheimer's disease. The polynucleotide of the invention can
CC be used in gene therapy. This sequence represents the protein sequence
CC identified by SwissProt Accession No: Q08469 relating to the sodium-
CC dependent neurotransmitter transporter protein of the invention.
XX
SQ Sequence 729 AA;

Query Match 65.1%; Score 2483; DB 23; Length 729;
Best Local Similarity 63.8%; Pred. No. 7.3e-246;
Matches 472; Conservative 110; Mismatches 134; Indels 24; Gaps 8;

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QY 1 MPKNSKVTOREHSHSEHVTESVADLLALEPVD--YKOSVLNVAGEAGQKQXAVEELDAE 58
Db 1 MPKNSKVVRD-LDDDVIEVSKDLSVEDSVKSKSELIVDQE-----EKDQDAE 52
QY 59 D-----RPANNSKIQYILAQIGFSGVLGNWIRFPYLCOKNGGGAYLPVLLVLIIGI 111
Db 53 DGEVDDERPAWNSKQYILAQIGFSGVLGNWIRFPYLCOKNGGGAYLPVLLVLIIGI 112
QY 112 PLFFLEAVGQIRRGISGVWHYICPRLGIGFSSICVLCFLVGLYVNIIGWSIFYPFKS 171
Db 113 PLFFLEAVGQIRRGISGVWHYICPRLGIGFSSICVLCFLVGLYVNIIGWSIFYPFKS 172
QY 172 FOYPLPWSCEPVVRNGSAVVEAECEKSSATTYFWYREALDISISSEGLNWKMTLCL 231
Db 173 FOQPLPWCQCLPVKNASHYIEPECESKSSATTYFWYREALDISISSEGLNWKMTGCL 232
QY 232 LVVWSIGGMAVGKIQSSGKVMYFSSLPVYVVLACFLVRGLLRGAVDGIILHMETPKLVK 291
Db 233 LAANVMVCLAMTKGQSSKIMYFSSLPVYVVLACFLVRGLLRGAVDGIILHMETPKLVK 292
QY 292 MLDPOVREVATQVFFGLGFGGIVFSSYNKQDNCHDFGALVSEFINFTSVLATLVV 351
Db 293 MLEPVWREAAQVFPALGFGGIVFSSYNKQDNCHDFGALVSEFINFTSVLATLVV 352
QY 352 FVVLGFKANIMKEKCVVENAEKILGYLNTNVLNRDLIPPHVNFESHLTKDYMEMDNVMT 411
Db 353 FAVLGFKANIVNEKICQNSEMILKLLKTGNVSDVIPRHINLSAVTAEDYHVYVDIIOK 412
QY 412 VKEDQFSAIGLDPCLLEDELKSVQGTGLAFIAFTAMTHFTSPFWSVMPFLMLNLGL 471
Db 413 VKEEFAVLHLKACQIEDELNAVOGTGLAFIAFTAMTHFTSPFWSVMPFLMLNLGL 472
QY 472 GSMITGAGITPIDTSKVPKEMFTVGCFTFLVGLLVQVRSGNYFTVMDYDYSATLP 531
Db 473 GSMFTGIEIIPVVDFTVRKELIIVICLLAFICLMEFVQVRSGNYFTVMDYDYSATLP 532
QY 532 LTLVILENIAVWIGPKKQWELTEMLGFRPYRFYVWKKFVSLPCLMAVLTIASIIQL 591
Db 533 LTLVILENIAVSVIGIDKLELDMGLFAPSKYIYVWKKYISPLMLVLTIASIVNM 592
QY 592 GVTTPAYSARIKEEAARYLFPNWPMAIITLIVVATLPVVFVLRHFLHLLSDGS-NT 650
Db 593 GLSPPGYNARIKEEAEFLSPMGMVVCFLMVLAILPVVVFVLRHFLHLLSDGS-NT 652
QY 651 LSVYTKKARMKDISMLENDETRFSLKVPSEAPSPMTHRSYLGPGSTSPLETSNPN 710
Db 653 ASVTYKGRVLEKPEVNL-DGDDASLIHGKIPSEMSSEFNFGKNIYKQSGSTLDTA--PN 709
QY 711 GPYGRGYLLA---STPSESL 727
Db 710 GRYGIGYLMADPMPDESLL 729
RESULT 8
AAE05100
ID AAE05100 standard; Protein; 675 AA.
XX
XX AAE05100;
XX
XX 18-SEP-2001 (first entry)
XX
XX Drosophila melanogaster dmNTT4 protein.
XX
XX Fruit fly; invertebrate symporter cell surface receptor; dmNTT4;
KW sodium/neurotransmitter family; SNF; biopesticide; therapy.
XX
XX Drosophila melanogaster.
XX
XX WO200149848-A2.
XX
XX 12-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US35551.
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XX
PR 30-DEC-1999; 99US-0173929.
PR 15-MAR-2000; 2000US-0189399.
PR 23-MAR-2000; 2000US-0191686.
PR 23-MAR-2000; 2000US-0191687.
PR 23-MAR-2000; 2000US-0191688.
PR 23-MAR-2000; 2000US-0191695.
XX (GENO-) GENOPTERA LLC.
XX
XX Kellerman KA, Keegan KP, Ebens AJ, Torpey J;
PI N-PSDB; AAD09680.
XX
XX WPI; 2001-441879/47.
XX
XX Novel invertebrate symporter cell surface receptor proteins and nucleic
acid encoding the protein useful as pesticide or drug target and to
identify compounds that have utility as therapeutics or pesticides -
XX
XX Claim 18; Page 59-61; 71pp; English.
XX
XX The invention relates to invertebrate symporter cell surface receptors
of the sodium/neurotransmitter family (SNF) and nucleic acid molecules
encoding such receptors. The SNF protein is useful for detecting a
candidate compound especially a putative pesticidal or pharmaceutical
agent that interacts with an invertebrate symporter cell surface
receptor protein or its fragment. Insect or worm genetically modified
to express protein of the invention is useful for studying invertebrate
symporter cell surface receptor protein activity, by detecting the
phenotype caused by the expression or mis-expression of the protein in
the animal. Nucleic acids encoding the invertebrate receptor protein or
their fragments are useful as biopesticides. SNF nucleic acids are
useful for generating mutant phenotypes in an animal model or living
cells that are used to study the regulation of genes encoding the
proteins which are useful as pesticide or drug targets. The genetically
modified organisms or cells are useful in screening assays to identify
pesticides or therapeutics and thus are useful in the identification of
new drug targets, therapeutic agents, diagnostics and prognostics
useful in treatment of disorders associated with ion channels. The
nucleic acid molecules are also useful as hybridisation probes.
XX The present sequence is Drosophila melanogaster (dm) NTT4 SNF
XX homologue which is referred as dmNTT4.
XX
XX Sequence 675 AA;
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```
Query Match 39.2%; Score 1495.5; DB 22; Length 675;
Best Local Similarity 44.0%; Pred. No. 2.8e-144;
Matches 279; Conservative 124; Mismatches 198; Indels 33; Gaps 6;
QY 59 DRPAWNSKQYILAQIGFSGVLGNWIRFPYLCOKNGGGAYLPVLLVLIIGIPLFLEL 118
Db 54 ERAAWSGKMOFFLSIIGYSVGLGNWIRFPYLCQNGGGAFIPFVMMLEIGIPLFLEL 113
QY 119 AVGORIRRGISGVWHYICPRLGIGFSSICVLCFLVGLYVNIIGWSIFYPFKSFOYPLPW 178
Db 114 GICQRLGALGVWNTIHPWLGIGISICVTLFVALYVNIITVWFFLFNSFRPLPW 173
QY 179 SECVPVVRNGSAVVEAECEKSSATTYFWYREALDISISSEGLNWKMTLCLLVVWSIG 238
Db 174 SSCPL--NGTGFELE-ECASSETYFWYRTTLDAAAPSDMPGGLKWNIVLCMLSWTIV 230
QY 239 GNAVKGIGQSSGKVMYFSSLPVYVVLACFLVRGLLRGAVDGIILHMETPKLVMLDPQW 298
Db 231 FFTVMKGIQSSGKVMYFSSLPVYVLTIFIRGITLRGAGAGLMHMTYTPKVEKLEPTVM 290
QY 299 REVATQVFFGLGFGGIVFSSYNKQDNCHDFGALVSEFINFTSVLATLVVFFVVLGFK 358
Db 291 LDATQVFFGLGFGGIVFSSYNKQDNCHDFGALVSEFINFTSVLATLVVFFVVLGFK 350
QY 359 ANIMNEKCVVENAE-----KILGYLNTNVLNRDLIPPHVNFESHLTKDYMEMDNVMTVK 413
Db 351 ATVNVDRCVASNTIILVKNKLLG-LN-----DFOGVEQAMSLN 388
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QY 414 EDQFSAIGLDPCLLEDELKSVQGTGLAFIAFTEAMTHFTSPFWSVMFFMLINLGLS 473
Db 389 GTELLRLQLSECSLAHELDNAEGTGLAFIVFTQAIVELPGAPFWAVLFFFTMLLSLGLS 448
QY 474 MIGHTMAGITTPIID--TSKVPKEMFTVGCCTFTPLVGLLFFVORSGNYFTVTFDDYSATL 530
Db 449 QIGLEGMCLTFLDIDIIRKVKKHQVTVGVLFCFIVGFICTGAGERYLWKFDFSGAGTI 508
QY 531 PLTLIVILENTAVAMIVGPKKFMQELTEMLGFRPYRFFYFMWKFVSPCLMAVLTASIIQ 590
Db 509 GLVVVALMEMIAVIFIGHERTEDIFQMTGYRPGRYQWWTWRYICPVMIVMCLVSSVVF 568
QY 591 LGVTPPAYSAWIKKEEAERYLYFNPWPMALLITLIVATLPIPVVFLRHFHLLSDGNT 650
Db 569 MVIENPTYGAWNADLMTEQSYNPNWVMGIALSMILAGVLPMPVFLMRSFOCLKVDLDI 628
QY 651 LSVYKKARKMKDISNLEENDETRFILSKVPSEA 684
Db 629 HQSIRNETTASTKEMIDNDDNNMSPDMPQDS 662

RESULT 9
ABB61363
ID ABB61363 standard; Protein; 744 AA.
XX AC ABB61363;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 10881.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX XX 27-SEP-2001.
XX XX 23-MAR-2001; 2001WO-US09231.
XX XX 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX XX (PEKE) PE CORP NY.
XX PA Venter JC, Adams M, Li PWD, Myers EW;
XX PI WPI; 2001-656860/75.
XX DR N-PSDB; ABL05466.
XX XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -
XX XX Disclosure; SEQ ID NO 10881; 21pp + Sequence Listing; English.
XX PS The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins
XX CC (ABB57737-ABB72072).
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX XX Sequence 744 AA;
XX SQ Query Match 39.2%; Score 1495.5; DB 22; Length 744;

Best Local Similarity 44.0%; Pred. No. 3.3e-144;
Matches 279; Conservative 124; Mismatches 198; Indels 33; Gaps 6;
QY 59 DRPAWSKLOYIIAQIGFSGVLGNIRFPYLCQKNGGAYLVYLVLLIIIGIPFLLEL 118
Db 54 ERAWSKMGQFFLSIIGYSVGLGNIRFPYLCQKNGGAYLVYLVLLIIIGIPFLLEL 113
QY 119 AVGORIRRSIGVWHYICPRGGIGFSSCIVCLFVGLVYNYVLIIGHSIEYFFKSFQYPLPW 178
Db 114 GIGORMLGAIVYNTIHPMLGGIGISCIIVTLFVLYNYVLIITWFFLYFNSFRYPDPW 173
QY 179 SECPVVRVGVAVVAEACEKSSATTYFYREALDISISSESGLNWKMTCLLVVMWSIG 238
Db 174 SSCPL--NGTGFLE-ECASSETTYFYRTTLDAAPSMDPGLKWLIVLCLMSWTIV 230
QY 239 GMVKGIGQSGKVMYFSSLPYVVLACFLVGLLRLRGAVDGILHMFPTKLVKMLDPQVM 298
Db 231 FFIVMKGIOSSGKVVYFTSLFPYIVLTITFFIRGITRGAGAGLHMHTPKVEKLEPTVM 290
QY 299 REVATQVFFGLGLGGFVGVIVFESSYNKONNCHDFGALVSFINFTSVLATLVVGVVLPK 358
Db 291 LDAATQVYFSGLAFGLSIAEFSYNTPKNNCVRDVLVSVCAVNAVITAVSVIFAILGPK 350
QY 359 ANIMNERKCVVENAE-----KILGYLNTNVLSDRLIPPHVNFSLTTKDYMEMDNVIMTYK 413
Db 351 ATVNVDRCVASNTIELVKNKLLG-LN-----DTQGYEQAMSLN 388
QY 414 EDQFSAIGLDPCLLEDELKSVQGTGLAFIAFTEAMTHFTSPFWSVMFFMLINLGLS 473
Db 389 GTELLRLQLSECSLAHELDNAEGTGLAFIVFTQAIVELPGAPFWAVLFFFTMLLSLGLS 448
QY 474 MIGHTMAGITTPIID--TSKVPKEMFTVGCCTFTPLVGLLFFVORSGNYFTVTFDDYSATL 530
Db 449 QIGLEGMCLTFLDIDIIRKVKKHQVTVGVLFCFIVGFICTGAGERYLWKFDFSGAGTI 508
QY 531 PLTLIVILENTAVAMIVGPKKFMQELTEMLGFRPYRFFYFMWKFVSPCLMAVLTASIIQ 590
Db 509 GLVVVALMEMIAVIFIGHERTEDIFQMTGYRPGRYQWWTWRYICPVMIVMCLVSSVVF 568
QY 591 LGVTPPAYSAWIKKEEAERYLYFNPWPMALLITLIVATLPIPVVFLRHFHLLSDGNT 650
Db 569 MVIENPTYGAWNADLMTEQSYNPNWVMGIALSMILAGVLPMPVFLMRSFOCLKVDLDI 628
QY 651 LSVYKKARKMKDISNLEENDETRFILSKVPSEA 684
Db 629 HQSIRNETTASTKEMIDNDDNNMSPDMPQDS 662

RESULT 10
AAG64193
ID AAG64193 standard; Protein; 616 AA.
XX AC AAG64193;
XX DT 19-OCT-2001 (first entry)
XX DE Human nerve mass-transferring protein.
XX KW Human; nerve mass-transferring protein.
XX OS Homo sapiens.
XX XX CN1287170-A.
XX PD 14-MAR-2001.
XX PF 08-SEP-1999; 99CN-0118725.
XX PR 08-SEP-1999; 99CN-0118725.
XX PA (UYFU-) UNIV FUDAN.
XX XX Yu L, Zhao Y, Zhang H;

XX WPI; 2001-398933/43.
DR N-PSDB; AAH73688.
XX New human nerve mass-transferring protein and its code sequence -
PT Claim 2; Page 17-19 (disclosure); 24pp; Chinese.
XX
CC The invention provides a cDNA sequence encoding a new human nerve
CC mass-transferring protein. The invention also relates to
CC the application of the polynucleotide and the polypeptide, and the
CC method of producing the polynucleotide and the polypeptide. The
CC present sequence is the protein of the invention.
XX
XX Sequence 616 AA;
SQ
Query Match 34.7%; Score 1323; DB 22; Length 616;
Best Local Similarity 41.7%; Pred. No. 1.4e-126;
Matches 263; Conservative 125; Mismatches 199; Indels 44; Gaps 11;
QY 25 LALEPVDYKQSVNLVAGAGGKQKAEELDAEDRPANWSKLOYILAQIGFSVGLGNW 84
Db 3 LAIKKPCSDPRAGAEABAGAMEKA-----RPLWANSLOQVFACISYAVGLGNW 53
QY 85 RPYLCQKNGGAYLPVYLVLIIIGIPLELAVGQIRRGSGVWHYICPRLGGIGF 144
Db 54 RPYLCQMGVGGSFVPIIIMLIVEGMPLLYLELAVGQRMQSGIGAWRTISPYLSGV 113
QY 145 SSCIVCLFVGLYNNYIIGWSIFEFKSFQYPLPWSCEPVRNGSVAVAECEKSSATTY 204
Db 114 ASVVVSFFLSMYNNVINAWAFYHFSFQDPLPWSVCPL--NGNHTGYDECEKASQY 171
QY 205 FMYREALDISDSISGGLNWKMTCLLVWSIGGMVAGKQSSGKVMYFSLFPYVVL 264
Db 172 FMYRTLNISSPQENGSGVQWEPALCLLAWLVVYLILRGTESTGKVVYFTASLPYCVL 231
QY 265 ACFLVRLGLRGAVGDIHMFPPKLVKMDPQWRREVATQVFGLGLGGVTVFSSYNK 324
Db 232 IYILIRGLTHGATNGLMYMFPPKIEOLANPKAWINAAQIFSLGLGSLIAPASYNE 291
QY 325 QDNCHFGALVSFNFTTSVLATLVVVLGFKANIMKCVVENAEKILGYLNTNVL 384
Db 292 PSNNQKHAIIIVSLINSETSFASIVTFSIYGKATFNENCL-----KKVSLLLTNTFD 346
QY 385 RDLIPPHVNFSLHTKDYMEMDNVMTVKEDQFSAL--GLDPCLEDELKSKVQGTGLAF 442
Db 347 -----LEDGFLTASNLEQVKYLASAYPSKISEMFPQKNCSELELDTAVQGTGLAF 399
QY 443 IAFTEAMTHPTSPFWSVNFLLMLINLGLSGMIGTMAGITTTIID-----TSKVPKEMFTV 498
Db 400 IVYTEAIKMEVSQSLWSVLYPFPMLMLGIGSMGLNGTAAITLPTLTDSKIISHLPKRAISG 459
QY 499 GCCVFTFLVGLLVQVRSNGVYFVTFMDEDDYSATPLPLIVILENIAMVIYGPKKFMOELTE 558
Db 460 LVLCVNCVAGVMTFMEAGNYFDIFNDYAATLSLLILVLETVIACVYVYGLRRFESDLKA 519
QY 559 MLGFRPYRFYFVWKFVSPCLMA---VLTASIIQLGVTPTPAYSAWIKKEAERYLY---612
Db 520 MTGRAVSWYKVMWAGVSPLLIVSLFVLYSDIYITGTL--KYQAW---DASOGQLVTMD 574
QY 613 FPNPMALLITLVVATLPIPV----VFVLR 639
Db 575 YPAVALAVIGLLVASSTWCIPLAALGTFVQR 605
RESULT 11
AAW73376
ID AAW73376 standard; Protein; 647 AA.
XX
AC AAW73376;
XX
DT 12-FEB-1999 (first entry)
XX

Human HPDDV78 protein sequence.
DE
XX HPDDV78; human; neurotransmitter; mutation detection; gene therapy;
KW brain hypoxia; seizure; stroke.
XX
OS Homo sapiens.
XX
PN EP881290-A2.
XX
PD 02-DEC-1998.
XX
PF 15-APR-1998; 98EP-0302907.
XX
PR 08-DEC-1997; 97EP-0309887.
PR 27-MAY-1997; 97GB-0010906.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
PA Brown AM, Evans JR;
XX WPI; 1999-001396/01.
DR N-PSDB; AAV08571.
XX
PT New neurotransmitter HPDDV78 polypeptides and polynucleotides -
PT useful as diagnostic reagents and for prevention and treatment of
PT brain hypoxia and stroke
XX
PS Claim 10; Page 19-20; 24pp; English.
XX
CC This sequence is the human neurotransmitter HPDDV78 polypeptide of
CC the invention. HPDDV78 polypeptides and polynucleotides are useful for
CC diagnosing susceptibility to diseases by detecting mutations in the
CC HPDDV78 gene using probes containing the HPDDV78 nucleotide sequence, and
CC can diagnose diseases associated with HPDDV78 imbalance by determining
CC HPDDV78 polypeptide expression levels. HPDDV78 polypeptides can
CC be used to screen for agonists and antagonists which bind HPDDV78
CC by observing the binding, or stimulation or inhibition of HPDDV78
CC activity. These can be used in treatment to activate (agonist)
CC or inhibit (antagonist) HPDDV78 activity, in addition to direct
CC administration of antisense sequences to prevent expression, or HPDDV78
CC polypeptides to treat conditions associated with a lack of HPDDV78
CC protein. Gene therapy may also be used to affect endogenous HPDDV78
CC polypeptide production. HPDDV78 antibodies are useful for inducing an
CC immune response to immunise and prevent diseases, and for isolating
CC HPDDV78 clones or purifying the polypeptide by affinity
CC chromatography. HPDDV78 polypeptides can be administered directly or as a
CC vaccine to inoculate against disease. Diseases diagnosed, prevented or
CC treated include: brain hypoxia, trauma, seizure and stroke. The HPDDV78
CC polypeptide is also useful for mapping the gene to a chromosome, allowing
CC gene inheritance to be studied through linkage analysis.
XX
SQ Sequence 647 AA;
Query Match 34.5%; Score 1318; DB 20; Length 647;
Best Local Similarity 42.4%; Pred. No. 4.9e-126;
Matches 260; Conservative 122; Mismatches 187; Indels 44; Gaps 11;
QY 43 EAGKQKQVABEELDAEDRPANWSKLOYILAQIGFSVGLNWRFPYLCQKNGGAYLPY 102
Db 52 EAGAMEKA-----RPLWANSLOQVFACISYAVGLGNWRFPYLCQMGGSFLVPY 102
QY 103 LVLLIIIGIPLELAVGQIRRGSGVWHYICPRLGGIGFSSCIVCLFVGLYNNYIIG 162
Db 103 IIMLIVEGMPLLYLELAVGQRMQSGIGAWRTISPYLSGVSVASVAVVVSFFLSMYNNVINA 162
QY 163 WSIFYFPEKSFQYPLPWSCEPVRNGSVAVAECEKSSATTYFMYREALDISDSISESG 222
Db 163 WAFWYLFHFSFQDPLPWSVCPL--NGNHTGDECEKASSTQYFWTKRTLNISSPQENG 220
QY 223 LNKMTLCILLVWSIGGMVAGKQSSGKVMYFSLFPYVYLACFLVRGLLIRGAVDGLL 282
Db 221 VQNEPALCLLAWLVVYLILRGTESTGKVVYFTASLPYCVLIYILIRGLTHGATNGLM 280

Db 363 MOQRNASDPAAYLAQVFOCTDINAFUSEAVEGTGLAFIVTEAITKMPLSPLMSVLEFI 422

QY 465 MLINLGLSGMIGTMAITTTIID----TSKVPKREMTVGCCVFTFLVGLLFEVQSRGNVYF 520

Db 423 MLEFCLGSSMFGNMGVVPLODLRVIPPKPKVGLGLICLGTFLIGFIETLNSGQXWL 482

QY 521 TMFDDYSATLPLILVILENIAMWYGPCKFMQELTEMLGFRPYRFFYMWKFSPLCM 580

Db 483 SLSDSVAGSIPLLIIAFCEMFVVVYGVDRFNKIDIEFMIGHKPNIFMQVTRVVSPLIM 542

QY 581 AVLTTSIIQGVTPPAYSAW---IKEEAERYLYFFNWPMLLITLIVATLPIP--VV 635

Db 543 LIILPFFVVEVSEQLTYSWDPGYEEFPKSKISYNWVYVVVVVIVAGVSLTIPGYAI 602

QY 636 FVLRHFLHSDGS-----NTLSVS 654

Db 603 YKLIRNHCQKPGDHQGLVSTLSTA 626

RESULT 14

ABB59777

ID ABB59777 standard; Protein: 662 AA.

AC ABB59777;

XX 26-MAR-2002 (first entry)

DT Drosophila melanogaster polypeptide SEQ ID NO 6123.

DE Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical.

KW Drosophila melanogaster.

OS WO200171042-A2.

PN 27-SEP-2001.

PD 23-MAR-2001; 2001WO-US09231.

PF 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

DR N-PSDB; ABL03880.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signalling and cell-cell

PT interactions -

XX Disclosure; SEQ ID NO 6123; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

XX capable of detecting 1000 or more genes from Drosophila. The invention is

XX useful in developmental biology and in elucidating cell signalling and

XX cell-cell interactions in higher eukaryotes for the development of

XX insecticides, therapeutics and pharmaceutical drugs. The invention

XX discloses genomic DNA sequences (ABLI6176-ABLI30511), expressed DNA

XX sequences (ABLI01840-ABLI16175) and the encoded proteins

XX (ABB57737-ABB72072).

XX The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 662 AA;

SQ Query Match 34.2%; Score 1305; DB 22; Length 662;

Best Local Similarity 40.7%; Pred. No. 1.1e-124;

Matches 248; Conservative 109; Mismatches 209; Indels 44; Gaps 4;

QY 34 KOSVLNAGEAGKQKXAVEEELDAEDRPANNSKLOYILAOIGFSVGLGNIRFPYLCOKN 93

Db 28 KAEIIVAIATASADQODIVEGEGERESWDSKIMFLLATIGYAVGLGNVWRFPYLAQKN 87

QY 94 GGGAYLVVPLVLLIIIGIPLFFLELAVGORIRRGSGIWHYICPRLGIGFSSICVLCUFV 153

Db 88 GGGAYLVVPLVLLIIIGIPIFYLELAIGORLRKGAIGWQSVQSPYLGIGISSAVSVIV 147

QY 154 GUYVNIIGWSIYFPFKSFQYPLPWCPCPV--VRNGSVAVVVEAECEKSSATYFYVREALD 212

Db 148 ALYVNTIIACWLYLLHSESPPLPWADCPTRLKYNFTYDHEPECVASSPTQFYWYRTTLQ 207

QY 213 ISDSISESGLNKMTLCILAVVNSIGMAVGKIOSGKVMYFSSLPYVYVVLACFLVRGL 272

Db 208 CSESVDMPENFNHMAIALIVSNFLVYICWQGITSSGKIYVMTAIPYVVLIIFFFRGI 267

QY 273 LLRGAVDGLHMFTPKLVKMLDPQVREVATQVFGLGLGFGGVIVFSSYNKQDNCHFD 332

Db 268 TLKGAADGVAHLFTPRWETLLDPVWLEAGTQIEFSLGLAFGLIAFSSYNPANNCYRD 327

QY 333 GALVSFINFTSVLATILVVFVGLFKANINNEKCVVENAEKILGLVINTNLSRDLIPPHV 392

Db 328 AILVSLTNCGTSMFAGVYVFSVIGFKATATPDRCETEERNGLVA-----Q 371

QY 393 NFSLHTTKDYEMDNVIMTVKEDQFSALGLDPCLLEDELDKSVQCTGLAFIAFTAMTHF 452

Db 372 NKTH-----NLPVCDLQTELANSASCTGLAFIAFTAINOF 407

QY 453 PTFSPFVSMFPLMLINLGLSGMIGTMAITTIIDTS---KVPKEMFTVGCVCVFTFLVGL 509

Db 408 PGAQLWAVLFLMLFTLIGIDSOFGTLEGVTSLVDMKLPNLPKEYIYVIGALCFSCOTISM 467

QY 510 LFVQSRGNYFVTMFDDYSATLPLILVILENIAMWYGPCKFMQELTEMLGFRPYRFFV 569

Db 468 CFANGAGSYIFQLMDSPAGNFPLLIIALFELCSISYITGVRRFSDDIEMWTGSRNFYWM 527

QY 570 YMKFVSPLCMAVLTTASIIQLGVTPPAYSAWIKKEAERYLYFFNWPMLLITLIVAT 629

Db 528 FCWKYLSPCAMVTILLASFYQLLTGSSYPAWIGSKGATEGMEWPHWCIVVAFLLISLI 587

QY 630 LPIPVVFLVR 639

Db 588 LWIPIVAVLR 597

RESULT 15

AAW07635

ID AAW07635 standard; Protein: 616 AA.

XX AAW07635;

XX 05-FEB-1997 (first entry)

XX Rat brain derived orphan transporter, rB21a.

XX Rat; brain; orphan; transporter; rB21a; identification; drug;

XX therapeutic agent; neurological; psychiatric; disorder;

XX alleviation; abnormality; treatment; migraine headache; swelling;

XX injury; hypoxia; seizure; stroke; probe; primer; detection;

XX therapy; production; transgenic animal; antibody; inhibition.

XX Rattus rattus.

XX Key Location/Qualifiers

XX FH 38..58

XX Domain /note= "putative transmembrane domain I"

XX FT 65..85

XX Domain /note= "putative transmembrane domain II"

XX FT 110..130

XX Domain /note= "putative transmembrane domain III"

XX FT 194..214

XX Domain /note= "putative transmembrane domain IV"

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 14:08:09 ; Search time 41 Seconds
(without alignments)
3653.567 Million cell updates/sec

Title: US-09-923-444A-2

Perfect score: 727

Sequence: 1 MPKNSKVTQREHSSEHVETES.....NPNPGYGRGYLLASTPESEL 727

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: SPTRMBL_21.*

2: sp_archaea.*

3: sp_bacteria.*

4: sp_fungi.*

5: sp_human.*

6: sp_invertebrate.*

7: sp_mammal.*

8: sp_mhc.*

9: sp_organelle.*

10: sp_plant.*

11: sp_rhodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	3.0	241	11 Q8ROC2	Q8ROC2 mus musculus
2	19	2.6	249	4 Q9NW50	Q9NW50 homo sapien
3	16	2.2	265	6 Q9XS32	Q9XS32 bos taurus
4	16	2.2	289	4 Q9H9F5	Q9H9F5 homo sapien
5	16	2.2	289	4 Q8TBM6	Q8TBM6 homo sapien
6	15	2.1	744	5 Q9V8I8	Q9V8I8 drosophila
7	14	1.9	397	4 Q9BYZ7	Q9BYZ7 homo sapien
8	14	1.9	577	11 Q9IXG6	Q9IXG6 mus musculus
9	14	1.9	615	11 Q88576	Q88576 mus musculus
10	14	1.9	628	4 Q96N87	Q96N87 homo sapien
11	13	1.8	615	11 Q62687	Q62687 rattus norv
12	12	1.7	674	5 Q8WPM9	Q8WPM9 oikopleura
13	11	1.5	502	16 Q9CMU0	Q9CMU0 pasteurilla
14	11	1.5	505	16 Q9K7C5	Q9K7C5 bacillus ha
15	11	1.5	511	16 Q9JXM3	Q9JXM3 neisseria m
16	11	1.5	511	16 Q9JWA5	Q9JWA5 neisseria m

17	11	1.5	614	5 Q9U2E3	Q9U2E3 caenorhabdi
18	10	1.4	102	5 Q9NF30	Q9NF30 caenorhabdi
19	10	1.4	527	16 Q9KQ16	Q9KQ16 vibrio chol
20	10	1.4	635	5 Q18288	Q18288 caenorhabdi
21	10	1.4	706	5 Q9XUG5	Q9XUG5 caenorhabdi
22	10	1.4	728	5 Q9U2E0	Q9U2E0 caenorhabdi
23	9	1.2	432	17 Q8TXS1	Q8TXS1 methanopyru
24	9	1.2	453	16 Q9KDT3	Q9KDT3 bacillus ha
25	9	1.2	489	17 Q8TOM2	Q8TOM2 methanosarc
26	9	1.2	518	13 Q9OWD3	Q9OWD3 oncorhynch
27	9	1.2	592	4 Q9NP91	Q9NP91 homo sapien
28	9	1.2	592	11 Q8VDB9	Q8VDB9 mus musculu
29	9	1.2	616	4 Q8TF10	Q8TF10 homo sapien
30	9	1.2	616	11 Q64093	Q64093 rattus norv
31	9	1.2	635	11 Q91WT6	Q91WT6 mus musculu
32	9	1.2	635	11 Q88575	Q88575 mus musculu
33	9	1.2	768	5 P90890	P90890 caenorhabdi
34	8	1.1	128	13 Q9DFY5	Q9DFY5 rana catesb
35	8	1.1	155	2 Q9Z5Y2	Q9Z5Y2 frankia sp.
36	8	1.1	174	8 Q9ME78	Q9ME78 drosophila
37	8	1.1	174	8 Q9ME49	Q9ME49 drosophila
38	8	1.1	174	8 Q9MD81	Q9MD81 drosophila
39	8	1.1	174	8 Q9MGW5	Q9MGW5 drosophila
40	8	1.1	174	8 Q9MGL6	Q9MGL6 drosophila
41	8	1.1	264	16 Q9PM93	Q9PM93 campylobact
42	8	1.1	318	16 Q9KMZ4	Q9KMZ4 vibrio chol
43	8	1.1	333	5 Q22352	Q22352 caenorhabdi
44	8	1.1	431	16 Q9RWL0	Q9RWL0 deinococcus
45	8	1.1	449	16 Q9CMM5	Q9CMM5 pasteurilla

ALIGNMENTS

RESULT 1

Q8ROC2	ID	Q8ROC2	PRELIMINARY;	PRT;	241 AA.
AC	Q8ROC2;				
DT	01-JUN-2002	(TrEMBLrel. 21, Created)			
DT	01-JUN-2002	(TrEMBLrel. 21, Last sequence update)			
DT	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)			
DE	Hypothetical 27.0 kDa protein (Fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=EYE;				
RA	Strausberg R.;				
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: BC027078; AAH27078.1; --				
KW	Hypothetical protein.				
FT	NON_TER				
SQ	SEQUENCE	241 AA; 27030 MW; AA15BDCBF5BBE07C CRC64;			

Query Match 3.0%; Score 22; DB 11; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.9e-14; Mismatches 0; Indels 0; Gaps 0;

QY	511	FVQRSGNYFVTMFDYSATLPL	532
Db	24	FVQRSGNYFVTMFDYSATLPL	45

RESULT 2

Q9NW50	ID	Q9NW50	PRELIMINARY;	PRT;	249 AA.
AC	Q9NW50;				
DT	01-OCT-2000	(TrEMBLrel. 15, Created)			
DT	01-OCT-2000	(TrEMBLrel. 15, Last sequence update)			
DT	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)			
DE	CDNA FLJ10316 fis, clone NT2RM2000422, highly similar to sodium- and				

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DE chloride-dependent transporter NTT73.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,
RA Niromiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK001178; BAA91536.1; -.
DR InterPro: IPR000175; Na/ntran_sympoort.
DR Pfam: PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSMPORT.
DR ProDom: PD000448; Na/ntran_sympoort; 2.
DR PROSITE; PS0267; NA_NEUROTRAN_SYMP_3; 1.
SQ SEQUENCE 249 AA; 27873 MW; 64395E571A377377 CRC64;

Query Match 2.6%; Score 19; DB 4; Length 249;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 435 VQGTGLAFIAFTEAMTHFP 453
DB 152 VQGTGLAFIAFTEAMTHFP 170
|||||

RESULT 3
Q9XS32 PRELIMINARY; PRT; 265 AA.
AC Q9XS32;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Orphan transporter short splicing variant.
GN BV7-3S3 OR BV7-3S2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Sakata K., Shimada S.;
RT "Orphan transporter.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB020857; BAA77226.1; -.
DR EMBL; AB020855; BAA77224.1; -.
DR EMBL; AB020856; BAA77225.1; -.
DR InterPro: IPR000175; Na/ntran_sympoort.
DR Pfam: PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSMPORT.
DR ProDom: PD000448; Na/ntran_sympoort; 1.
DR PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; 1.
DR PROSITE; PS0267; NA_NEUROTRAN_SYMP_3; 1.
SQ SEQUENCE 265 AA; 29687 MW; 20F95214D2AD26F9 CRC64;

Query Match 2.2%; Score 16; DB 6; Length 265;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 WRPPLYCQKNGGGAYL 99
DB 85 WRPPLYCQKNGGGAYL 100
|||||

RESULT 4
Q9XS32 PRELIMINARY; PRT; 265 AA.
AC Q9XS32;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Orphan transporter short splicing variant.
GN BV7-3S3 OR BV7-3S2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Sakata K., Shimada S.;
RT "Orphan transporter.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB020857; BAA77226.1; -.
DR EMBL; AB020855; BAA77224.1; -.
DR EMBL; AB020856; BAA77225.1; -.
DR InterPro: IPR000175; Na/ntran_sympoort.
DR Pfam: PF00209; SNF; 1.
DR PRINTS; PR00176; NANEUSMPORT.
DR ProDom: PD000448; Na/ntran_sympoort; 1.
DR PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; 1.
DR PROSITE; PS0267; NA_NEUROTRAN_SYMP_3; 1.
SQ SEQUENCE 265 AA; 29687 MW; 20F95214D2AD26F9 CRC64;

Query Match 2.2%; Score 16; DB 4; Length 289;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 WRPPLYCQKNGGGAYL 99
DB 85 WRPPLYCQKNGGGAYL 100
|||||

RESULT 5
Q8TBM6 PRELIMINARY; PRT; 289 AA.
AC Q8TBM6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 32.2 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT TISSUE=BRAIN;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022253; AAH2253.1; -.
DR KW Hypothetical protein.
SQ SEQUENCE 289 AA; 32248 MW; AB0768DB5574BF47 CRC64;

Query Match 2.2%; Score 16; DB 4; Length 289;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 WRPPLYCQKNGGGAYL 99
DB 85 WRPPLYCQKNGGGAYL 100
|||||

RESULT 6
Q9V8I8 PRELIMINARY; PRT; 744 AA.
ID Q9V8I8
AC Q9V8I8;

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DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE CG5226 protein.
 GN CG5226.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., M.G.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003799; AAF57678.1;
 DR FlyBase; FBgn0034355; CG5226.
 DR InterPro; IPR000175; Na/ntran_symport.
 DR Pfam; PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR ProDom; PD000448; Na/ntran_symport; 2.
 DR PROSITE; PS00610; NA_NEUOTRAN_SYMP_1; 1.
 DR PROSITE; PS0267; NA_NEUOTRAN_SYMP_3; 1.
 SQ SEQUENCE 744 AA; 82953 MW; ED4A742B3E0E483B CRC64;

Query Match 2.1%; Score 15; DB 5; Length 744;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 SVGLNWRFPYLCQ 91
 DB 72 SVGLNWRFPYLCQ 86
 |||||||||||||

RESULT 7
 Q9BYZ7

ID Q9BYZ7 PRELIMINARY; PRT; 397 AA.
 AC Q9BYZ7;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Sodium channel-like protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homiq.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Londono-Vallejo J.A.;
 RT "Sequence of a BAC carrying the entire hTERT gene.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY007685; AAC23290.1;
 DR InterPro; IPR000175; Na/ntran_symport.
 DR Pfam; PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR ProDom; PD000448; Na/ntran_symport; 1.
 DR PROSITE; PS0267; NA_NEUOTRAN_SYMP_3; 1.
 SQ SEQUENCE 397 AA; 43784 MW; E70588E4D7FD9CF6 CRC64;

Query Match 1.9%; Score 14; DB 4; Length 397;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 VGLGNWRFPYLCQ 91
 DB 36 VGLGNWRFPYLCQ 49
 |||||||||||||

RESULT 8
 Q91XG6 PRELIMINARY; PRT; 577 AA.
 ID Q91XG6
 AC Q91XG6;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Similar to X transporter protein 2.
 GN XTRP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC010748; AAH10748.1;
 DR MGI; MGI:1336892; Xtrp2.
 DR InterPro; IPR000175; Na/ntran_symport.
 DR Pfam; PF00209; SNF; 1.
 DR ProDom; PD000448; Na/ntran_symport; 2.
 DR PROSITE; PS0267; NA_NEUOTRAN_SYMP_3; 1.
 SQ SEQUENCE 577 AA; 65254 MW; 5F84F7C5CF1B14E3 CRC64;

Query Match 1.9%; Score 14; DB 11; Length 577;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 VGLGNWRFPYLCQ 91
 DB 35 VGLGNWRFPYLCQ 48
 |||||||||||||

RESULT 9
 Q88576 PRELIMINARY; PRT; 615 AA.
 ID Q88576
 AC Q88576; O88577; O88578; O88579; O88580; O88581;
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)

RP MEDLINE=95029937; PubMed=7943364;
 RC Wasserman J.C., Delpire E., Tonidandel W., Kojima R., Gullans S.R.;
 RA "Molecular characterization of ROSIT, a renal osmotic stress-induced
 RT Na(-)-Cl(-)-organic solute cotransporter";
 RL Am. J. Physiol. 267:F688-F694(1994).
 DR EMBL; U12973; AAC13771.1; -
 DR InterPro: IPR000175; Na/ntran_sympoort.
 DR Pfam: PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR ProDom; PD000448; Na/ntran_sympoort; 2.
 DR PROSITE; PS00267; NA_NEUOTRAN_SYMP_3; 1.
 SQ SEQUENCE 615 AA; 69556 MW; F41E7DELDC276918 CRC64;

Query Match 1.8%; Score 13; DB 11; Length 615;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 VGLGNIWRFPYLC 90
 Db 35 VGLGNIWRFPYLC 47
 |||||

RESULT 12

Q8WPM9 PRELIMINARY; PRT; 674 AA.
 ID Q8WPM9
 AC Q8WPM9
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Similar to glycine transporter.
 GN BAC001.6.
 OS Oikopleura dioica.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;
 OC Oikopleuridae; Oikopleura.
 OX NCBI_TaxID=34765;
 RN [1]
 RP SEQUENCE FROM N.A., Edvardsen R.B., Jensen M.F., Beck A., Spriet E.,
 RA Seo H.C., Kube M., Thompson E.M., Lehrach H., Reinhardt R., Chourrout D.;
 RA "The marine chordate Oikopleura dioica has a miniature genome";
 RL Science 0:0-0(2001).
 DR EMBL; AF374376; AAL56437.1; -
 DR InterPro: IPR000175; Na/ntran_sympoort.
 DR Pfam; PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR ProDom; PD000448; Na/ntran_sympoort; 1.
 DR PROSITE; PS00610; NA_NEUOTRAN_SYMP_1; UNKNOWN_1.
 DR PROSITE; PS0267; NA_NEUOTRAN_SYMP_3; 1.
 SQ SEQUENCE 674 AA; 75155 MW; 9D318B6B54416E6 CRC64;

Query Match 1.7%; Score 12; DB 5; Length 674;
 Best Local Similarity 100.0%; Pred. No. 0.0024;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 VGLGNIWRFPYL 89
 Db 97 VGLGNIWRFPYL 108
 |||||

RESULT 13

Q9CMU0 PRELIMINARY; PRT; 502 AA.
 ID Q9CMU0
 AC Q9CMU0
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical protein PM0718.
 GN PM0718.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]

SEQUENCE FROM N.A.

RP STRAIN=PM70;
 RC MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida pm70";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 DR EMBL; AF006109; AAK02802.1; -
 DR InterPro: IPR000175; Na/ntran_sympoort.
 DR Pfam; PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR ProDom; PD000448; Na/ntran_sympoort; 1.
 DR PROSITE; PS00610; NA_NEUOTRAN_SYMP_1; 1.
 DR PROSITE; PS0267; NA_NEUOTRAN_SYMP_3; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 502 AA; 53982 MW; 06ADEE74DECF1107 CRC64;

Query Match 1.5%; Score 11; DB 16; Length 502;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 VGLGNIWRFPY 88
 Db 26 VGLGNIWRFPY 36
 |||||

RESULT 14

Q9K7C5 PRELIMINARY; PRT; 505 AA.
 ID Q9K7C5
 AC Q9K7C5
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Sodium-dependent transporter.
 GN BH3439.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fujii F., Hirakawa C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001518; BAB07158.1; -
 DR InterPro: IPR000175; Na/ntran_sympoort.
 DR Pfam; PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR ProDom; PD000448; Na/ntran_sympoort; 1.
 DR PROSITE; PS00610; NA_NEUOTRAN_SYMP_1; 1.
 DR PROSITE; PS0267; NA_NEUOTRAN_SYMP_3; 1.
 KW Complete proteome.
 SQ SEQUENCE 505 AA; 54296 MW; 607C0F6A00D67B07 CRC64;

Query Match 1.5%; Score 11; DB 16; Length 505;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 VGLGNIWRFPY 88
 Db 20 VGLGNIWRFPY 30
 |||||

RESULT 15

Q9JXM3 PRELIMINARY; PRT; 511 AA.
 ID Q9JXM3
 AC Q9JXM3
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Sodium-and chloride-dependent transporter.
 GN NMB1975.
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_taxID=491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC58 / SEROGROUP B;
 RX MEDLINE=2017555; PubMed=10710307;
 RA Tetelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
 RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
 RA Gill J., Scarlato V., Maignani V., Pizza M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 RT MC58.";
 RL Science 287:1809-1815(2000).
 DR EMBL; AE002546; AAF42303.1; -.
 DR TIGR; NMB1975; -.
 DR InterPro; IPR000175; Na/ntran_sympor.
 DR Pfam; PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR ProDom; PD000448; Na/ntran_sympor; 1.
 DR PROSITE; PS00610; NA_NEUOTRAN_SYMP_1; 1.
 DR PROSITE; PS0267; NA_NEUOTRAN_SYMP_3; 1.
 KW Complete proteome.
 SQ SEQUENCE 511 AA; 54905 MW; 270B4E731EE7ALDD CRC64;

Query Match 1.5%; Score 11; DB 16; Length 511;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 VGLGNWRRPPY 88
 Db | | | | | | | | | |
 27 VGLGNWRRPPY 37

Search completed: April 21, 2003, 14:11:06
 Job time : 45 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 14:07:19 ; Search time 14 Seconds
(without alignments)
2153.806 Million cell updates/sec

Title: US-09-923-444A-2

Perfect score: 727

Sequence: 1 MPKNKVTQREHSHSVETES.....NPNPGYGRGYLLASTPESEL 727

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size: 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	11.4	727	1	P31662 rattus norv
2	52	7.2	439	1	Q9h1v8 homo sapien
3	51	7.0	225	1	Q28001 bos taurus
4	22	3.0	729	1	Q9xs59 bos taurus
5	22	3.0	729	1	Q08469 rattus norv
6	22	3.0	730	1	Q9h217 homo sapien
7	11	1.5	508	1	P44849 haemophilus
8	11	1.5	615	1	Q03614 caenorhabdi
9	9	1.2	518	1	O42563 oncorhynch
10	9	1.2	630	1	O35899 cavia porce
11	9	1.2	630	1	O60857 mus musculu
12	9	1.2	630	1	P31652 rattus norv
13	9	1.2	636	1	Q99884 homo sapien
14	9	1.2	637	1	P28573 rattus norv
15	8	1.1	174	1	S6A7_HUMAN
16	8	1.1	174	1	NU6M_DROJA
17	8	1.1	611	1	YD19_METJA
18	8	1.1	690	1	YCR3_YEAST
19	8	1.1	1278	1	ATK6_STNY3
20	7	1.0	73	1	NPCI_HUMAN
21	7	1.0	107	1	P41130 photorhabd
22	7	1.0	112	1	P40097 saccharomyc
23	7	1.0	135	1	Q99ml8 mus musculu
24	7	1.0	158	1	P08860 oryza sativ
25	7	1.0	174	1	P18317 klebsiella
26	7	1.0	174	1	P18933 drosophila
27	7	1.0	215	1	Q92xx5 papio hamad
28	7	1.0	231	1	P35402 arabidopsis
29	7	1.0	250	1	P33373 escherichia
30	7	1.0	252	1	P34120 dictyosteli
31	7	1.0	279	1	Q01019 herpesvirus
32	7	1.0	314	1	P41794 salmonella
33	7	1.0	315	1	Q92j38 helicobacte
					O26091 helicobacte

RESULT 1

ID	NTT4_RAT	STANDARD;	PRT;	727 AA.
AC	P31662;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Orphan sodium- and chloride-dependent neurotransmitter transporter NTT4.			
GN	NTT4.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=93114444; PubMed=8093354;			
RA	Liu Q.-R., Mandiyan S., Lopez-Corcuera B., Nelson H., Nelson N.;			
RT	"A rat brain cDNA encoding the neurotransmitter transporter with an unusual structure.";			
RL	FEBS Lett. 315:114-118(1993).			
RP	[2]			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=94125086; PubMed=8294906;			
RA	el Mestikawy S., Giros B., Pohl M., Hamon M., Kingsmore S.F.,			
RT	Seidin M.F., Caron M.G.;			
RT	"Characterization of an atypical member of the Na+/Cl(-)-dependent transporter family: chromosomal localization and distribution in GABAergic and glutamatergic neurons in the rat brain.";			
RL	J. Neurochem. 62:445-455(1994)			
CC	-!- FUNCTION: NOT YET KNOWN, ORPHAN TRANSPORTER.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-!- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CENTRAL NERVOUS SYSTEM AND IS MORE ABUNDANT IN THE CEREBELLUM AND THE CEREBRAL CORTEX.			
CC	-!- SIMILARITY: BELONGS TO THE SODIUM-NEUROTRANSMITTER SYMPORTER FAMILY (SNF).			
CC	-----			
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CC	-----			
CC	EMBL; L06434; AAB24776.1; -			
DR	EMBL; S68944; AAC60673.1; -			
DR	PIR; S27043; S27043			
DR	InterPro; IPR000175; Na/ntran_symport.			
DR	Pfam; PF00209; SNF; 1.			
DR	PRINTS; PR00176; NANEUSMPORT.			
DR	ProDom; PD000448; Na/ntran_symp; 2.			
DR	PROSITE; PS00610; NA-NEUROTRAN_SYMP_1; 1.			
DR	PROSITE; PS00754; NA-NEUROTRAN_SYMP_2; 1.			

Q9pj96 chlamydia m
P56444 capra hircu
P56447 ovibos mosc
O19037 ovibos aries
P75910 escherichia
P13720 escherichia
P57449 buchnera ap
O06545 homo sapien
Q00421 mus musculu
P17499 autographa
Q9uxer7 sulfolobus
P57757 mus musculu

ALIGNMENTS

DR PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.
 KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
 KW Symport.

DOMAIN 1 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 1 (POTENTIAL).
 FT TRANSMEM 97 116 2 (POTENTIAL).
 FT TRANSMEM 141 161 3 (POTENTIAL).
 FT DOMAIN 162 224 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 225 243 4 (POTENTIAL).
 FT TRANSMEM 252 269 5 (POTENTIAL).
 FT TRANSMEM 305 322 6 (POTENTIAL).
 FT TRANSMEM 334 355 7 (POTENTIAL).
 FT DOMAIN 356 451 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 452 471 8 (POTENTIAL).
 FT TRANSMEM 495 513 9 (POTENTIAL).
 FT TRANSMEM 529 549 10 (POTENTIAL).
 FT TRANSMEM 570 591 11 (POTENTIAL).
 FT TRANSMEM 619 641 12 (POTENTIAL).
 FT DOMAIN 642 727 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 393 393 Y -> C (IN REF. 2).
 FT CONFLICT 261 261 G -> S (IN REF. 2).
 FT CONFLICT 499 499
 SQ SEQUENCE 727 AA; 81055 MW; C676048C0A6BDF7C CRC64;

Query Match 11.4%; Score 83; DB 1; Length 727;
 Best Local Similarity 100.0%; Pred. No. 6.2e-76;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 EEELDAEDRPAWNSKLYLAQIGFSGVGLGNWIRPPYLCQKNGGGAYLPVLLVLIIGI 111
 DB 52 EEELDAEDRPAWNSKLYLAQIGFSGVGLGNWIRPPYLCQKNGGGAYLPVLLVLIIGI 111

QY 112 PLFLELAVGQIRIRGSGVWHY 134
 DB 112 PLFLELAVGQIRIRGSGVWHY 134

RESULT 2
 NNT4_HUMAN
 ID NNT4_HUMAN STANDARD; PRT; 439 AA.
 AC Q9H1V8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Orphan sodium- and chloride-dependent neurotransmitter transporter
 DE NNT4 (Fragment).
 GN NNT4
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Clark G.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: NOT YET KNOWN, ORPHAN TRANSPORTER.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE SODIUM-NEUROTRANSMITTER SYMPORTER FAMILY (SNF).
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 CC
 CC EMBL; AL137790; CAC19682.1; ALT_INIT.
 CC InterPro; IPR000175; Na/ntran_symport.
 CC Pfam; PF00209; SNF; 1.
 CC PRINTS; PR00176; NANEUSNPRT.

DR PRODOM; PD000448; Na/ntran_symport; 2.
 DR PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; PARTIAL.
 DR PROSITE; PS00754; NA_NEUROTRAN_SYMP_2; PARTIAL.
 DR PROSITE; PS0267; NA_NEUROTRAN_SYMP_3; 1.
 KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
 KW Symport.

NON_TER 1 1
 FT TRANSMEM 17 34 6 (POTENTIAL).
 FT TRANSMEM 46 67 7 (POTENTIAL).
 FT DOMAIN 68 163 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 164 183 8 (POTENTIAL).
 FT TRANSMEM 207 225 9 (POTENTIAL).
 FT TRANSMEM 241 261 10 (POTENTIAL).
 FT TRANSMEM 282 303 11 (POTENTIAL).
 FT TRANSMEM 331 353 12 (POTENTIAL).
 FT DOMAIN 354 439 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 439 AA; 49011 MW; 44634308C281C740 CRC64;

Query Match 7.2%; Score 52; DB 1; Length 439;
 Best Local Similarity 100.0%; Pred. No. 1.4e-44;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 VLGFKANIMNEKCVVENAEKILGYLNTNVLSDRLIPPHVNFSLTKDYMEM 405
 DB 66 VLGFKANIMNEKCVVENAEKILGYLNTNVLSDRLIPPHVNFSLTKDYMEM 117

RESULT 3
 NNT4_BOVIN
 ID NNT4_BOVIN STANDARD; PRT; 225 AA.
 AC Q28001;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Orphan sodium- and chloride-dependent neurotransmitter transporter
 DE NNT4 (Fragment).
 GN NNT4
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jones E.M.C.;
 RL Tissue=Retina;
 CC
 CC "Sodium- and chloride-dependent neurotransmitter transporters in bovine
 CC retina: identification and localization by in situ hybridization
 CC histochemistry.";
 CC Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: NOT YET KNOWN, ORPHAN TRANSPORTER.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE SODIUM-NEUROTRANSMITTER SYMPORTER
 CC FAMILY (SNF).
 CC
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 CC EMBL; U19593; AAA61578.1;
 CC InterPro; IPR000175; Na/ntran_symport.
 CC Pfam; PF00209; SNF; 1.
 CC PRODOM; PD000448; Na/ntran_symport; 1.
 CC PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; 1.
 CC PROSITE; PS00754; NA_NEUROTRAN_SYMP_2; 1.
 CC PROSITE; PS0267; NA_NEUROTRAN_SYMP_3; 1.
 KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
 KW Symport.

FT	TRANSMEM	335	356	7 (POTENTIAL).
FT	DOMAIN	357	452	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	453	472	8 (POTENTIAL).
FT	TRANSMEM	496	514	9 (POTENTIAL).
FT	TRANSMEM	530	550	10 (POTENTIAL).
FT	TRANSMEM	571	592	11 (POTENTIAL).
FT	TRANSMEM	620	642	12 (POTENTIAL).
FT	DOMAIN	643	729	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	187	187	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	213	213	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	383	383	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	394	394	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	729 AA;	81681 MW;	332FD83349C196A9 CRC64;

Query Match 3.0%; Score 22; DB 1; Length 729;
 Best Local Similarity 100.0%; Pred. No. 7.2e-14; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0;

QY	511	FVQRSGNYFVTMFDDYSATLPL	532
DB	512	FVQRSGNYFVTMFDDYSATLPL	533

RESULT 5
 ID NTT7_RAT STANDARD; PRT; 729 AA.
 AC Q08469; Q63838;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Orphan sodium- and chloride-dependent neurotransmitter transporter
 DE Orphan sodium- and chloride-dependent neurotransmitter transporter
 DE NT73 (Orphan transporter v7-3).
 GN NT73.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 ON NCBI_TaxID=10116;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93180651; PubMed=1363329;
 RA Uhl G.R., Kitayama S., Gregor P., Nanthakumar E., Persico A.M.,
 RA Shimada S.;
 RA 'Neurotransmitter transporter family cDNAs in a rat midbrain library:
 RT 'Orphan transporters' suggest sizeable structural variations.';
 RL Brain Res. Mol. Brain Res. 16:353-359(1992).
 CC -1- FUNCTION: NOT YET KNOWN, ORPHAN TRANSPORTER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
 CC FAMILY (SNF).
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 CC -----
 CC EMBL; L22022; AAA41729.1; -;
 CC EMBL; S56968; AAB25532.1; -;
 CC InterPro; IPR000175; Na/ntran_symport.
 CC Pfam; PF00209; SNF; 1.
 CC PRINTS; PR00176; NANEUSMPORT.
 CC PRODOM; PD000448; Na/ntran_symport; 2.
 CC PROSITE; PS00610; NA_NEUROTRAN_SYMPT_1;
 CC PROSITE; PS00754; NA_NEUROTRAN_SYMPT_2; FALSE_NEG.
 CC PROSITE; PS02674; NA_NEUROTRAN_SYMPT_3; 1.
 CC Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
 KW Domain.
 KW Symport.
 FT DOMAIN 1 69 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 70 90 1 (POTENTIAL).
 FT TRANSMEM 98 117 2 (POTENTIAL).

FT TRANSMEM 142 162 3 (POTENTIAL).
FT DOMAIN 163 225 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 226 244 4 (POTENTIAL).
FT TRANSMEM 253 270 5 (POTENTIAL).
FT TRANSMEM 306 323 6 (POTENTIAL).
FT TRANSMEM 335 356 7 (POTENTIAL).
FT DOMAIN 357 422 8 (POTENTIAL).
FT TRANSMEM 453 472 9 (POTENTIAL).
FT TRANSMEM 496 514 10 (POTENTIAL).
FT TRANSMEM 530 550 11 (POTENTIAL).
FT TRANSMEM 571 592 12 (POTENTIAL).
FT DOMAIN 643 729 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 1 3 MPK -> IP (IN REF. 1; AAB25532).
SQ SEQUENCE 729 AA; 81596 MW; ECDDC6403741B53E CRC64;

Query Match 3.0%; Score 22; DB 1; Length 729;
Best Local Similarity 100.0%; Pred. No. 7.2e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 FVQRSGNYFVTMFDDYSATLPL 532
DB 512 FVQRSGNYFVTMFDDYSATLPL 533
|||||
RESULT 6
ID NT77_HUMAN STANDARD; PRT; 730 AA.
AC Q9H2J7;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Orphan sodium- and chloride-dependent neurotransmitter transporter
DE NT773 (Orphan transporter v7-3).
GN NT773.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RX MEDLINE=20564208; PubMed=11112352;
RA Farmer M.K., Robbins M.J., Medhurst A.D., Campbell D.A., Ellington K.,
RA Duckworth M., Brown A.M., Middlemiss D.N., Price G.W., Pangalos M.N.;
RT "Cloning and characterization of human NT75 and v7-3: two orphan
RT transporters of the Na(+)/Cl(-)-dependent neurotransmitter
RL Genomics 70:241-252(2000).
CC -1- FUNCTION: NOT YET KNOWN, ORPHAN TRANSPORTER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
CC FAMILY (SNF).
CC
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CC or send an email to license@lsb-sib.ch).
CC
CC EMBL: AF265577; AAC41361.1; -.
CC InterPro: IPR000175; Na/nttran_symport.
CC Pfam: PF00209; SNF; 1.
CC PRINTS: PR00176; NANEUSMPORT.
CC DR PRODOM: PD000448; Na/nttran_symport; 2.
CC DR PROSITE: PS00610; NA_NEUROTRAN_SYMP_1; 1.
CC DR PROSITE: PS00754; NA_NEUROTRAN_SYMP_2; FALSE_NEG.
CC DR PROSITE: PS00267; NA_NEUROTRAN_SYMP_3; 1.

KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
KW Sympor.
FT DOMAIN 1 69 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 70 90 1 (POTENTIAL).
FT TRANSMEM 98 117 2 (POTENTIAL).
FT TRANSMEM 142 162 3 (POTENTIAL).
FT DOMAIN 163 225 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 226 244 4 (POTENTIAL).
FT TRANSMEM 253 270 5 (POTENTIAL).
FT TRANSMEM 306 323 6 (POTENTIAL).
FT TRANSMEM 335 356 7 (POTENTIAL).
FT DOMAIN 357 452 8 (POTENTIAL).
FT TRANSMEM 453 472 9 (POTENTIAL).
FT TRANSMEM 496 514 10 (POTENTIAL).
FT TRANSMEM 530 550 11 (POTENTIAL).
FT TRANSMEM 571 592 12 (POTENTIAL).
FT DOMAIN 643 730 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 730 AA; 81836 MW; 45963118E06CFF6 CRC64;

Query Match 3.0%; Score 22; DB 1; Length 730;
Best Local Similarity 100.0%; Pred. No. 7.2e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 FVQRSGNYFVTMFDDYSATLPL 532
DB 512 FVQRSGNYFVTMFDDYSATLPL 533
|||||
RESULT 7
Y736_HAEIN STANDARD; PRT; 508 AA.
ID Y736_HAEIN
AC P44849;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical sodium-dependent transporter H10736.
GN H10736.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bq / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fletschmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Utterback T.R., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Fine L.D., Friedman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RL Science 269:496-512(1995).
CC -1- FUNCTION: PUTATIVE SODIUM-DEPENDENT TRANSPORTER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
CC FAMILY (SNF).
CC
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CC EMBL; U32757; AAC22395.1; -
CC TIGR; H10736; -
DR InterPro: IPR000175; Na/ntran_symport.
DR Pfam: PF00209; SNF; 1.
DR Prodom: PD000448; Na/ntran_symport; 1.
DR PROSITE; PS00610; NA_NEUROTAN_SYM_1; 1.
DR PROSITE; PS00754; NA_NEUROTAN_SYM_2; FALSE_NEG.
DR PROSITE; PS00267; NA_NEUROTAN_SYM_3; 1.
KW Hypothetical protein; Transport; Transmembrane; Symport;
KW Complete proteome.
FT TRANSMEM 19 39 POTENTIAL.
FT TRANSMEM 47 67 POTENTIAL.
FT TRANSMEM 92 112 POTENTIAL.
FT TRANSMEM 153 173 POTENTIAL.
FT TRANSMEM 186 206 POTENTIAL.
FT TRANSMEM 228 248 POTENTIAL.
FT TRANSMEM 272 292 POTENTIAL.
FT TRANSMEM 325 345 POTENTIAL.
FT TRANSMEM 365 385 POTENTIAL.
FT TRANSMEM 394 414 POTENTIAL.
FT TRANSMEM 432 452 POTENTIAL.
FT TRANSMEM 469 489 POTENTIAL.
SQ SEQUENCE 508 AA; 55177 MW; 5CC50526DE854BB9 CRC64;

Query Match 1.5%; Score 11; DB 1; Length 508;

Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 VGLGNWRFPY 88

DB 29 VGLGNWRFPY 39

|||||||

RESULT 8

NTDO_CAEEL
ID NTDO_CAEEL STANDARD; PRT; 615 AA.
AC Q03614; Q9XTK0;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium-dependent dopamine transporter (DA transporter) (DAT).
GN T23G5.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98440631; PubMed=9765501;
RA Jayanthi L.D.; Apparsundaram S.; Malone M.D.; Ward E.; Miller D.M.;
RA Eppler M.; Blakely R.D.;
RT "The Caenorhabditis elegans gene T23G5.5 encodes an antidepressant-and cocaine-sensitive dopamine transporter.";
RL Mol. Pharmacol. 54:601-609(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R.; Alnsough R.; Anderson K.; Baynes C.; Berks M.;
RA Bonfield J.; Burton J.; Connell M.; Copsey T.; Cooper J.; Coulson A.;
RA Craxton M.; Dear S.; Du Z.; Durbin R.; Favell A.; Fraser A.;
RA Fulton L.; Gardner A.; Green P.; Hawkins T.; Hillier L.; Jier M.;
RA Johnston L.; Jones M.; Kershaw J.; Kirsten J.; Laister N.;
RA Latreille P.; Lightning J.; Lloyd C.; Mortimore B.; O'Callaghan M.;
RA Parsons J.; Percy C.; Rifkin L.; Roopra A.; Saunders D.; Showkneen R.;
RA Sims M.; Smalton N.; Smith A.; Smith M.; Sonhammer E.; Staden R.;
RA Sulston J.; Thierry-Mieg J.; Thomas K.; Vaudin M.; Vaughan K.;
RA Waterston R.; Watson A.; Weinstock L.; Wilkinson-Sproat J.;
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";

RL Nature 368:32-38(1994).
RN [3]
RP REVISIONS.
RA Durbin R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TERMINATES THE ACTION OF DOPAMINE BY ITS HIGH AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
CC -!- SIMILARITY: BELONGS TO THE SODIUM:NEUROTANSMITTER SYMPORTER FAMILY (SNF).
CC -----
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CC -----
CC EMBL; AF079899; AAC83661.1; -
CC EMBL; Z19158; CAA79575.2; -
CC EMBL; Z19156; CAA79575.2; JOINED.
CC EMBL; Z19156; CAA79564.2; -
CC EMBL; Z19158; CAA79564.2; JOINED.
CC PIR; S28306; S28306.
CC WormPep: T23G5.5; CE25124.
CC InterPro: IPR000175; Na/ntran_symport.
CC Pfam: PF00209; SNF; 1.
CC PRINTS; PR00176; NANEUSMPORT.
CC Prodom: PD000448; Na/ntran_symport; 2.
CC PROSITE; PS00610; NA_NEUROTAN_SYM_1; 1.
CC PROSITE; PS00754; NA_NEUROTAN_SYM_2; 1.
CC PROSITE; PS00267; NA_NEUROTAN_SYM_3; 1.
KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
KW Symport.
FT DOMAIN 1 48 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 49 69 1 (POTENTIAL).
FT TRANSMEM 74 94 2 (POTENTIAL).
FT TRANSMEM 125 145 3 (POTENTIAL).
FT DOMAIN 146 232 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 233 253 4 (POTENTIAL).
FT TRANSMEM 258 278 5 (POTENTIAL).
FT TRANSMEM 344 364 6 (POTENTIAL).
FT TRANSMEM 371 391 7 (POTENTIAL).
FT TRANSMEM 393 413 8 (POTENTIAL).
FT TRANSMEM 440 460 9 (POTENTIAL).
FT TRANSMEM 462 482 10 (POTENTIAL).
FT TRANSMEM 515 535 11 (POTENTIAL).
FT TRANSMEM 550 570 12 (POTENTIAL).
FT DOMAIN 571 615 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 162 162 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 615 AA; 69265 MW; 0DA2876EB3AC8049 CRC64;
Query Match 1.5%; Score 11; DB 1; Length 615;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 80 LGNIWRFPYLC 90
DB 60 LGNIWRFPYLC 70
|||||||
RESULT 9
CP3R_ONCMY
ID CP3R_ONCMY STANDARD; PRT; 518 AA.
AC 042563;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome P450 3A27 (EC 1.14.14.1) (CYPIIA27).

GN CYP3A27.
 OS Oncochrynochus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Shasta; TISSUE=Liver;
 RX MEDLINE=99045386; PubMed=9826429;
 RA Lee S.-J., Wang-Buhler J.-L., Cok I., Yu T.S., Yang Y.H.,
 RA Miranda C.L., Lech J., Buhler D.R.;
 RT "Cloning, sequencing, and tissue expression of CYP3A27, a new member
 RT of the CYP3A subfamily from embryonic and adult rainbow trout
 RT livers.";
 RL Arch. Biochem. Biophys. 360:53-61(1998).
 CC -!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
 CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
 CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
 CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
 CC ACIDS, AND XENOBIOTICS.
 CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 CC oxidized flavoprotein + H(2)O.
 CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
 CC -!- INDUCTION: P450 CAN BE INDUCED TO HIGH LEVELS IN LIVER AND OTHER
 CC TISSUES BY VARIOUS FOREIGN COMPOUNDS, INCLUDING DRUGS, PESTICIDES,
 CC AND CARCINOGENS.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

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 DR EMBL; U96077; AAB82422.1; -;
 DR HSP; P14779; LJP2.
 DR InterPro: IPR001128; Cytochrome_P450.
 DR Pfam: PF00067; P450; 1.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 DR Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KW Microsome; Endoplasmic reticulum.
 FT BINDING 447 447
 FT SEQUENCE 518 AA; 59210 MW; 9B93AA12E617D0DF CRC64;
 Query Match 1.2%; Score 9; DB 1; Length 518;
 Best Local Similarity 100.0%; Pred. No. 0.91;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 619 ALLITLIV 627
 Db 17 ALLITLIV 25
 RESULT 10
 ID S6A4_CAVPO STANDARD; PRT; 630 AA.
 AC O35899;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Sodium-dependent serotonin transporter (5HT transporter) (5HTT).
 GN SLC6A4.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestinal mucosa;

RX MEDLINE=96180949; PubMed=8601815;
 RA Wade P.R., Chen J., Jaffe B., Kassam I.S., Blakely R.D., Gershon M.D.;
 RT "Localization and function of a 5-HT transporter in crypt epithelia
 RT of the gastrointestinal tract.";
 RL J. Neurosci. 16:2352-2364(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestinal mucosa;
 RA Chen J., Wade P.R., Rothman T.P., Gershon M.D.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS HIGH
 CC AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
 CC STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
 CC -!- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
 CC FAMILY (SNF).

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 DR EMBL; U84498; AAB82737.1; -;
 DR InterPro: IPR002437; 5HT_transporter.
 DR InterPro: IPR000175; Na/ntran_symport.
 DR Pfam; PF00209; SNF; 1.
 DR Pfam; PF03491; 5HT_transporter; 1.
 DR PRINTS; PR00176; NANEUSMPORT.
 DR PRODOM; PD000448; Na/ntran_symport; 1.
 DR PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; 1.
 DR PROSITE; PS00754; NA_NEUROTRAN_SYMP_2; 1.
 DR PROSITE; PS0267; NA_NEUROTRAN_SYMP_3; 1.
 DR Neurotransmitter transport; Transmembrane; Glycoprotein;
 KW Symport.
 KW DOMAIN 1 87 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 88 108 1 (POTENTIAL).
 FT TRANSMEM 116 135 2 (POTENTIAL).
 FT TRANSMEM 160 180 3 (POTENTIAL).
 FT DOMAIN 181 252 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 253 271 4 (POTENTIAL).
 FT TRANSMEM 280 297 5 (POTENTIAL).
 FT TRANSMEM 333 350 6 (POTENTIAL).
 FT TRANSMEM 362 383 7 (POTENTIAL).
 FT TRANSMEM 417 436 8 (POTENTIAL).
 FT TRANSMEM 464 482 9 (POTENTIAL).
 FT TRANSMEM 498 518 10 (POTENTIAL).
 FT TRANSMEM 539 558 11 (POTENTIAL).
 FT TRANSMEM 577 595 12 (POTENTIAL).
 FT DOMAIN 596 630 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 208 208 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 217 217 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 630 AA; 70113 MW; EE2A717DD9926D2F CRC64;
 Query Match 1.2%; Score 9; DB 1; Length 630;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 80 LGNIWRFPY 88
 Db 99 LGNIWRFPY 107
 RESULT 11
 ID S6A4_MOUSE STANDARD; PRT; 630 AA.
 AC Q60857; O35241;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Sodium-dependent serotonin transporter (5HT transporter) (5HTT).
GN SLC6A4 OR HTT OR SET.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9718261; PubMed=9037532;
RA Chang A.S., Chang S.M., Starnes D.M., Schroeter S., Bauman A.L.,
RA Blakely R.D.;
RT "Cloning and expression of the mouse serotonin transporter.";
RN Brain Res. Mol. Brain Res. 43:185-192(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129;
RA Bengel D., Hells A., Petri S., Seemann M., Glatz K., Andrews A.,
RA Murphy D.L., Lesch K.P.;
RT "Gene structure and 5'-flanking regulatory region of the murine
serotonin transporter.";
RN Brain Res. Mol. Brain Res. 44:286-292(1997).
RN [3]
RP SEQUENCE OF 1-114 FROM N.A.
RX STRAIN=BALB/c;
RA Saito N., Sakai N., Kobayashi S., Fujimoto M., Morikawa O.,
RA Ikegaki N.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 69-630 FROM N.A.
RX MEDLINE=93283858; PubMed=8507984;
RA Gregor P., Patel A., Shimada S., Lin C.L., Rochelle J.M., Kitayama S.,
RA Seldin M.F., Uhl G.R.;
RT "Murine serotonin transporter: sequence and localization to
chromosome 11.";
RL Mamm. Genome 4:283-284(1993).
CC -!- FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS HIGH
AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
CC -!- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
FAMILY (SNF).
CC -!- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 195.
CC -----
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CC -----
DR EMBL; AF013604; AAB67172.1; -;
DR EMBL; Y08870; CAA70092.1; -;
DR EMBL; Y08871; CAA70092.1; JOINED.
DR EMBL; Y08872; CAA70092.1; JOINED.
DR EMBL; Y08873; CAA70092.1; JOINED.
DR EMBL; Y08874; CAA70092.1; JOINED.
DR EMBL; Y08875; CAA70092.1; JOINED.
DR EMBL; Y08876; CAA70092.1; JOINED.
DR EMBL; Y08877; CAA70092.1; JOINED.
DR EMBL; Y08878; CAA70092.1; JOINED.
DR EMBL; Y08879; CAA70092.1; JOINED.
DR EMBL; Y08880; CAA70092.1; JOINED.
DR EMBL; U26452; AAA84750.1; -;
DR EMBL; X66119; -; NOT_ANNOTATED_CDS.
DR MGD; MGI:96285; SLC6A4.
DR InterPro; IPR002437; 5HT_transporter.
DR InterPro; IPR000175; Na/ntn_symport.
DR Pfam; PF00209; SNF; 1.
DR Pfam; PF03491; 5HT_transporter; 1.

DR PRINTS; PR00176; NANEUSMPORT.
DR ProDom; PD000448; Na/ntn_symport; 1.
DR PROSITE; PS00610; NA_NEUOTRAN_SYMPT_1;
DR PROSITE; PS00754; NA_NEUOTRAN_SYMPT_2;
DR PROSITE; PS00267; NA_NEUOTRAN_SYMPT_3;
KW Neurotransmitter transport; Transport; Glycoprotein;
KW Symport.
FT DOMAIN 1 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 108 1 (POTENTIAL).
FT TRANSMEM 116 135 2 (POTENTIAL).
FT TRANSMEM 160 180 3 (POTENTIAL).
FT DOMAIN 181 252 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 253 271 4 (POTENTIAL).
FT TRANSMEM 280 297 5 (POTENTIAL).
FT TRANSMEM 333 350 6 (POTENTIAL).
FT TRANSMEM 362 383 7 (POTENTIAL).
FT TRANSMEM 417 436 8 (POTENTIAL).
FT TRANSMEM 464 482 9 (POTENTIAL).
FT TRANSMEM 498 518 10 (POTENTIAL).
FT TRANSMEM 539 558 11 (POTENTIAL).
FT TRANSMEM 577 595 12 (POTENTIAL).
FT DOMAIN 596 630 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 217 217 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 196 196 P -> Q (IN REF. 2).
FT CONFLICT 415 415 A -> R (IN REF. 2).
SQ SEQUENCE 630 AA; 70147 MW; F37FE1EC1764FB30 CRC64;
Query Match 1.2%; Score 9; DB 1; Length 630;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 80 LGNIWRFPY 88
| | | | | | | | | |
DB 99 LGNIWRFPY 107
RESULT 12
S6A4_RAT STANDARD; PRT; 630 AA.
ID S6A4_RAT
AC P31652; P23976;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sodium-dependent serotonin transporter (5HT transporter) (5HTT).
GN SLC6A4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Wistar;
RC MEDLINE=92111740; PubMed=1765155;
RA Mayser W., Betz H., Schloss P.;
RT "Isolation of cDNAs encoding a novel member of the neurotransmitter
transporter gene family.";
RL FEBS Lett. 295:203-206(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain stem;
RX MEDLINE=92049754; PubMed=1944572;
RA Blakely R.D., Berson H.E., Fremeau R.T. Jr., Caron M.G., Peek M.M.,
RA Prince H.K., Bardley C.C.;
RT "Cloning and expression of a functional serotonin transporter from
rat brain.";
RL Nature 354:66-70(1991).
RN [3]
RP REVISIONS.
RC TISSUE=Brain stem;
RA Blakely R.D.;
RN Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RN [4]

RP SEQUENCE FROM N.A.
 RX MEDLINE=92054541; PubMed=1948036;
 RA Hoffman B.J., Mezey E., Brownstein M.J.;
 RT "Cloning of a serotonin transporter affected by antidepressants."; Science 254:579-580(1991).
 RL [5]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Fawn hooded;
 RC Gonzalez A.M., Smith A.P.L., Emery C.J., Higenbottom T.W.;
 RA Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RL
 CC -!- FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS HIGH AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
 CC -!- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER FAMILY (SNF).
 CC
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 CC
 DR EMBL; X63995; CAA45401.1; -
 DR EMBL; X63253; CAA44913.1; -
 DR EMBL; M79450; AAA42186.1; -
 DR EMBL; Y11024; CAA71909.1; -
 DR PIR; S30604; S30604.
 DR PIR; S19585; S19585.
 DR InterPro; IPR002437; 5HT_transporter.
 DR InterPro; IPR000175; Na/ntran_symport.
 DR Pfam; PF00209; SNF; 1.
 DR PRINTS; PR00176; NANEUSMPORF.
 DR PRODOM; PD000448; Na/ntran_symport; 1.
 DR PROSITE; PS00610; NA_NEUROTRAN_SYM_1; 1.
 DR PROSITE; PS00754; NA_NEUROTRAN_SYM_2; 1.
 DR PROSITE; PS0267; NA_NEUROTRAN_SYM_3; 1.
 KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein; Symport.
 KW DOMAIN 1 87 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 88 108
 FT TRANSMEM 116 135
 FT TRANSMEM 160 180
 FT DOMAIN 181 252 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 253 271
 FT TRANSMEM 280 297
 FT TRANSMEM 333 350
 FT TRANSMEM 362 383
 FT TRANSMEM 417 436
 FT TRANSMEM 464 482
 FT TRANSMEM 498 518
 FT TRANSMEM 539 558
 FT TRANSMEM 577 595
 FT DOMAIN 596 630 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 217 217 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 415 415 PGWF -> GMV (IN REF. 4).
 FT CONFLICT 533 536 PCGDIRMNAV -> RVGHPHCCVTHPRGHLFPATSLSS
 FT CONFLICT 621 630 KPTGLLL (IN REF. 4).
 SQ SEQUENCE 630 AA; 70171 MW; 44DA7C5888C403EE CRC64;

Query Match 1.2%; Score 9; DB 1; Length 630;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 LGNIWRFFY 88
 |||||
 Db 99 LGNIWRFFY 107

RESULT 13
 S6A7_HUMAN STANDARD; PRT; 636 AA.
 ID S6A7_HUMAN
 AC Q99884;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Sodium-dependent proline transporter.
 GN SLC6A7 OR PROT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RX MEDLINE=95379780; PubMed=7651355;
 RA Shafqat S., Velaz-Faircloth M., Henzi V.A., Whitney K.D., Yang-Feng T.L., Seldin M.F., Fremeau R.T. Jr.;
 RT "Human brain-specific L-proline transporter: molecular cloning, functional expression, and chromosomal localization of the gene in human and mouse genomes."; Mol. Pharmacol. 48:219-229(1995).
 RL
 CC -!- FUNCTION: TERMINATES THE ACTION OF PROLINE BY ITS HIGH AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: BRAIN.
 CC -!- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER FAMILY (SNF).
 CC
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 CC
 DR EMBL; S80071; AAB47007.2; -
 DR Genew; HGNC:11054; SLC6A7.
 DR MIM; 606205; -
 DR InterPro; IPR000175; Na/ntran_symport.
 DR Pfam; PF00209; SNF; 1.
 DR PRODOM; PD000448; Na/ntran_symport; 1.
 DR PROSITE; PS00610; NA_NEUROTRAN_SYM_1; 1.
 DR PROSITE; PS00754; NA_NEUROTRAN_SYM_2; 1.
 DR PROSITE; PS0267; NA_NEUROTRAN_SYM_3; 1.
 KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein; Symport; Amino-acid transport; Polymorphism.
 KW DOMAIN 1 45 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 46 66
 FT TRANSMEM 74 93
 FT TRANSMEM 117 137
 FT DOMAIN 138 214 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 215 233
 FT TRANSMEM 242 259
 FT TRANSMEM 295 312
 FT TRANSMEM 324 345
 FT TRANSMEM 378 397
 FT TRANSMEM 425 443
 FT TRANSMEM 459 479
 FT TRANSMEM 500 519
 FT TRANSMEM 538 556
 FT DOMAIN 557 636
 FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 345 345 L -> V (IN DBSNP:1468564).
 SQ SEQUENCE 636 AA; 70892 MW; 9A2D1071F59E409B CRC64;

Query Match 1.2%; Score 9; DB 1; Length 636;
 Best Local Similarity 100.0%; Pred. No. 1.1;

Query Match 1.2%; Score 9; DB 1; Length 637;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 GIPLFFLEL 118
|||||
DB 87 GIPLFFLEL 95

RESULT 15

NU6M_DROYA STANDARD; PRT; 174 AA.
AC P07709;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 6 (EC 1.6.5.3).
GN ND6.
OS Drosophila yakuba (Fruit fly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7245;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2317.6 Ivory Coast;
RX MEDLINE=86089137; PubMed=3001325;
RA Clary D.O., Wolstenholme D.R.;
RT "The mitochondrial DNA molecular of Drosophila yakuba: nucleotide
sequence, gene organization, and genetic code.";
RL J. Mol. Evol. 22:252-271(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84221393; PubMed=6328435;
RA Clary D.O., Wahleithner J.A., Wolstenholme D.R.;
RT "Sequence and arrangement of the genes for cytochrome b, URF1, URF4L,
URF4, URF5, URF6 and five tRNAs in Drosophila mitochondrial DNA.";
RL Nucleic Acids Res. 12:3747-3762(1984).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X03240; CAA26995.1; -
CC PIR; B30020; B30020.
CC Flybase: FBgn0013187; Dyak\mt:ND6.
CC InterPro; IPR001457; Oxidored_q3.
CC Pfam; PF00499; Oxidored_q3; 1.
CC Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 174 AA; 20200 MW; 469DA42041574C57 CRC64;

Query Match 1.1%; Score 8; DB 1; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 LLITLIV 627
|||||
DB 152 LLITLIV 159

Search completed: April 21, 2003, 14:10:18
Job time : 17 secs

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 GIPLFFLEL 118
|||||
DB 87 GIPLFFLEL 95

RESULT 14

SA67_RAT STANDARD; PRT; 637 AA.
AC P28573;
DT 01-DEC-1992 (Rel. 24, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sodium-dependent proline transporter.
GN SLC6A7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=92265305; PubMed=1350201;
RA Fremieu R.T. Jr., Caron M.G., Blakely R.D.;
RT "Molecular cloning and expression of a high affinity L-proline
transporter expressed in putative glutamatergic pathways of rat
brain.";
RL Neuron 8:915-926(1992).
CC -1- FUNCTION: TERMINATES THE ACTION OF PROLINE BY ITS HIGH AFFINITY
CC SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN SUBPOPULATIONS OF PUTATIVE
CC GLUTAMATERGIC PATHWAYS OF RAT BRAIN.
CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
CC FAMILY (SNF).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M88111; AAA41541.1; ALT_TERM.
CC InterPro; IPR000175; Na/ntran_symport.
CC Pfam; PF00209; SNF; 1.
CC PRINTS; PR00176; NAMEUSMPORT.
CC ProDom; PD000448; Na/ntran_symport; 1.
CC PROSITE; PS00610; NA_NEUROTRAN_SYMPT_1; 1.
CC PROSITE; PS00754; NA_NEUROTRAN_SYMPT_2; 1.
CC PROSITE; PS02067; NA_NEUROTRAN_SYMPT_3; 1.
CC Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
CC Symport; Amino-acid transport.
FT DOMAIN 1 45
FT TRANSMEM 46 66
FT TRANSMEM 74 93
FT TRANSMEM 117 137
FT DOMAIN 138 214
FT TRANSMEM 215 233
FT TRANSMEM 242 259
FT TRANSMEM 295 312
FT TRANSMEM 324 345
FT TRANSMEM 378 397
FT TRANSMEM 425 443
FT TRANSMEM 459 479
FT TRANSMEM 500 519
FT TRANSMEM 538 556
FT DOMAIN 557 637
FT CARBOHYD 182 182
FT N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 637 AA; 71090 MW; 9627E6DD5B9C9408 CRC64;

Result No.	Score	Query Match	Length	DB	ID	Description
1	83	11.4	727	2	S27043	neurotransmitter t
2	83	11.4	727	2	S15606	Na+/Cl(-)-dependen
3	33	4.5	33	2	C46027	neurotransmitter t
4	22	3.0	728	2	I65413	sodium-dependent n
5	22	3.0	730	2	S12632	sodium-dependent n
6	11	1.5	499	2	S28306	hypothetical prote
7	11	1.5	505	2	G84079	sodium-dependent t
8	11	1.5	508	2	G64089	probable transport
9	11	1.5	511	2	E81964	probable sodium-de
10	11	1.5	511	2	H81019	sodium- and chlori
11	11	1.5	579	2	D88551	protein T23G5.5 [l
12	11	1.5	615	2	T43330	catecholamine tran
13	10	1.4	527	2	E82127	sodium-dependent t
14	10	1.4	635	2	T20910	hypothetical prote
15	10	1.4	706	2	T20052	hypothetical prote
16	9	1.2	453	2	H83790	sodium-dependent t
17	9	1.2	607	2	S19585	serotonin transport
18	9	1.2	616	2	S50988	transporter protei
19	9	1.2	630	2	S30604	neurotransmitter t
20	9	1.2	637	2	JH0674	L-proline transpor
21	9	1.2	768	2	T22758	hypothetical prote
22	8	1.1	174	2	B30020	NADH2 dehydrogenas
23	8	1.1	264	2	D81253	probable peptide A
24	8	1.1	318	2	E82493	conserved hypothet
25	8	1.1	431	2	B73491	proton/sodium-glut
26	8	1.1	491	2	B69499	sodium- and chlori
27	8	1.1	492	2	F64464	sodium-dependent n
28	8	1.1	521	2	AP9549	amino acid permeas
29	8	1.1	611	2	S19434	probable transport

Db 52 EEELDAEDPAWNSKLOYIAQAIGFVGLGNWRFPYLCQKNGGAYLPVLLVLLIIGI 111
QY 112 PLFFLELAVGORIRRGSGVWHY 134
Db 112 PLFFLELAVGORIRRGSGVWHY 134

RESULT 3

C46027
neurotransmitter transporter - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Aug-1998
C:Accession: C46027
R:Liou, Q.R.; Mandiyan, S.; Nelson, H.; Nelson, N.
Proc. Natl. Acad. Sci. U.S.A. 89, 6639-6643, 1992
A:Title: A family of genes encoding neurotransmitter transporters.
A:Reference number: A46027; MUID:92335351; PMID:1631167
A:Accession: C46027
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-33 <LIU>
A>Note: sequence extracted from NCBI backbone (NCBIN:108827, NCBIP:108828)
C:Superfamily: gamma-aminobutyric acid transporter

Query Match 4.5%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 WNSKLYIAQAIGFVGLGNWRFPYLCQKNGG 95

Db 1 WNSKLYIAQAIGFVGLGNWRFPYLCQKNGG 33

RESULT 4

I65413
sodium-dependent neurotransmitter transporter - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Aug-1999
C:Accession: I65413
R:Uhl, G.R.; Kitayama, S.; Gregor, P.; Nanthakumar, E.; Persico, A.; Shimada, S.
Brain Res. Mol. Brain Res. 16, 353-359, 1992
A:Title: Neurotransmitter transporter family cDNAs in a rat midbrain library: 'orphan' transporter.
A:Reference number: I52632; MUID:93180651; PMID:1363329
A:Accession: I65413
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-728 <RES>
A:Cross-references: GB:S56968; NID:g298323; PIDN:AAB25532.1; PID:g298324
C:Superfamily: gamma-aminobutyric acid transporter

Query Match 3.0%; Score 22; DB 2; Length 728;
Best Local Similarity 100.0%; Pred. No. 7.6e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 FVORSGNYFVTMFDDYSATLPL 532

Db 511 FVORSGNYFVTMFDDYSATLPL 532

RESULT 5

I52632
sodium-dependent neurotransmitter transporter - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 21-Aug-1998
C:Accession: I52632
R:Uhl, G.R.; Kitayama, S.; Gregor, P.; Nanthakumar, E.; Persico, A.; Shimada, S.
Brain Res. Mol. Brain Res. 16, 353-359, 1992
A:Title: Neurotransmitter transporter family cDNAs in a rat midbrain library: 'orphan' transporter.
A:Reference number: I52632; MUID:93180651; PMID:1363329
A:Accession: I52632
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-730 <RES>
A:Cross-references: GB:S56141; NID:g298325
C:Superfamily: gamma-aminobutyric acid transporter

Query Match 3.0%; Score 22; DB 2; Length 730;
Best Local Similarity 100.0%; Pred. No. 7.6e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 FVORSGNYFVTMFDDYSATLPL 532

Db 513 FVORSGNYFVTMFDDYSATLPL 534

RESULT 6

S28306
hypothetical protein T2365.5 - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 21-Aug-1998
C:Accession: S28306
R:Berks, M.
submitted to the EMBL Data Library, December 1992

A:Reference number: S28296
A:Accession: S28306
A:Molecule type: DNA

A:Residues: 1-499 <BER>

A:Cross-references: EMBL:Z19158

C:Genetics:

A:Introns: 27/3; 134/2; 184/2; 215/3; 253/2; 332/3; 375/3; 409/1; 442/3

C:Superfamily: gamma-aminobutyric acid transporter

Query Match 1.5%; Score 11; DB 2; Length 499;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 LGNIWRFPYLC 90

Db 41 LGNIWRFPYLC 51

RESULT 7

G84079
sodium-dependent transporter BH3439 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: G84079
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fujii, F.; Masui, N.;

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: G84079

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-505 <STO>

A:Cross-references: GB:AP001518; GB:BA000004; NID:gl0175792; PIDN:BA07158.1; GSPDB:

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH3439

C:Superfamily: gamma-aminobutyric acid transporter

Query Match 1.5%; Score 11; DB 2; Length 505;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 VGLGNIWRFPY 88

Db 20 VGLGNIWRFPY 30

RESULT 8

E84089
probable transport protein HI0736 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 20-Aug-1999

C:Accession: E64089
 R:Plieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:Accession: E64089
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-508 <TIGR>
 A:Cross-references: GB:U32757; GB:I42023; NID:g1573740; PIDN:AAC22395.1; PID:g1573742; T
 C:Superfamily: gamma-aminobutyric acid transporter
 C:Keywords: transmembrane protein

Query Match 1.5%; Score 11; DB 2; Length 508;

Best Local Similarity 100.0%; Pred. No. 0.014; Mismatches 0; Indels 0; Gaps 0;

QY 78 VGLGNIWRFPY 88
 Db 29 VGLGNIWRFPY 39
 |||||

RESULT 9

E81964
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: E81964
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, P.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: A81775; MUID:20222556; PMID:10761919

A:Accession: E81964

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-511 <PAR>

A:Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83765.1; PID:g737921

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: NMA0470

C:Superfamily: gamma-aminobutyric acid transporter

Query Match 1.5%; Score 11; DB 2; Length 511;

Best Local Similarity 100.0%; Pred. No. 0.014; Mismatches 0; Indels 0; Gaps 0;

QY 78 VGLGNIWRFPY 88
 Db 27 VGLGNIWRFPY 37
 |||||

RESULT 10

H81019
 C:Species: Neisseria meningitidis
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C:Accession: H81019
 R:Tettelin, H.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Hickey, E.K.; Haft, D.H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M. Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V. A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: H81019

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-511 <TET>

A:Cross-references: GB:AE002546; GB:AE002098; NID:g7227234; PIDN:AAP42303.1; PID:g722723

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB1975

C:Superfamily: gamma-aminobutyric acid transporter

Query Match 1.5%; Score 11; DB 2; Length 511;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 VGLGNIWRFPY 88
 Db 27 VGLGNIWRFPY 37
 |||||

RESULT 11

D88551
 protein T23G5.5 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
 C:Accession: D88551

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999

A:Accession: D88551

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-579 <SPO>

A:Cross-references: GB:chr_III; PIDN:CAA79564.1; PID:g3879264; GSPDB:GN00021; CESP

A:Note: similar to sodium:neurotransmitter symporter

C:Genetics:

A:Gene: T23G5.5

A:Map position: 3

C:Superfamily: gamma-aminobutyric acid transporter

Query Match 1.5%; Score 11; DB 2; Length 579;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 LGNIWRFPYLC 90
 Db 41 LGNIWRFPYLC 51
 |||||

RESULT 12

T43330

catecholamine transport protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000

C:Accession: T43330

R:Jayanthi, L.D.; Apparsundaram, S.; Malone, M.D.; Ward, E.; Miller, D.M.; Eppler,

Mol. Pharmacol. 54, 601-609, 1998

A:Title: The Caenorhabditis elegans gene T23G5.5 encodes an antidepressant- and

A:Reference number: Z22431; MUID:98440631; PMID:9765501

A:Accession: T43330

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-615 <JAY>

A:Cross-references: EMBL:AF079899; NID:g3982784; PIDN:AAC83661.1; PID:g3982785

C:Genetics:

A:Note: T23G5.5

C:Superfamily: gamma-aminobutyric acid transporter

Query Match 1.5%; Score 11; DB 2; Length 615;

Best Local Similarity 100.0%; Pred. No. 0.017;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 LGNIWRFPYLC 90
 Db 60 LGNIWRFPYLC 70
 |||||

RESULT 13

E82127
sodium-dependent transporter VC2012 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: E82127
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.
I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: E82127
A:Status: preliminary
A:Map position: 1
A:Molecule type: DNA
A:Residues: 1-527 <HEI>
A:Cross-references: GB:AE004276; GB:AE003852; NID:g9656555; PIDN:AAF95160.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2012
A:Map position: 1
C:Superfamily: gamma-aminobutyric acid transporter

Query Match 1.4%; Score 10; DB 2; Length 527;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 VGLGNIWRFPY 88

Db 63 VGLGNIWRFPY 72

RESULT 14

T20910
hypothetical protein ZK1010.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T20910; T27646
R:McMurray, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19345
A:Accession: T20910
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-635 <WIL>
A:Cross-references: EMBL:Z81503; PIDN:CAB04115.1; GSPDB:GN00021; CESP:ZK1010.9
A:Experimental source: Clone F14F7
R:Gardner, A.
Submitted to the EMBL Data Library, November 1996
A:Reference number: Z20398
A:Accession: T27646
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-635 <W12>
A:Cross-references: EMBL:Z82083; PIDN:CAB04975.1; GSPDB:GN00021; CESP:ZK1010.9
A:Experimental source: clone ZK1010
C:Genetics:
A:Gene: CESP:ZK1010.9
A:Map position: 3
A:Introns: 71/3; 184/3; 403/1; 444/3; 547/3; 577/3
C:Superfamily: gamma-aminobutyric acid transporter

Query Match 1.4%; Score 10; DB 2; Length 635;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 VGLGNIWRFP 87

Db 83 VGLGNIWRFP 92

RESULT 15

T20052
hypothetical protein C49C3.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T20052
R:Mortimore, B.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19218
A:Accession: T20052
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-706 <WIL>
A:Cross-references: EMBL:Z82264; PIDN:CAB05153.1; GSPDB:GN00022; CESP:C49C3.1
A:Experimental source: clone C49C3
C:Genetics:
A:Gene: CESP:C49C3.1
A:Map position: 4
A:Introns: 50/3; 80/1; 125/1; 206/1; 240/2; 287/3; 325/3; 365/3; 487/3; 521/1; 564/3
C:Superfamily: gamma-aminobutyric acid transporter

Query Match 1.4%; Score 10; DB 2; Length 706;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 VGLGNIWRFP 87

Db 62 VGLGNIWRFP 71

Search completed: April 21, 2003, 14:11:37
Job time : 28 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 14:11:10 ; Search time 43 Seconds
(without alignments)
1278.402 Million cell updates/sec

Title: US-09-923-444A-2
Perfect score: 727
Sequence: 1 MPKSKVTOREHSEHWTES.....NPNQPYGRVILLASTPESEL 727

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 288829 seqs, 75613885 residues

Word size : 0

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : PublishedApplications_AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
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 - 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	727	100.0	727	10	US-09-923-444A-2
2	22	3.0	729	10	US-09-741-149-4
3	22	3.0	730	9	US-10-156-239-5
4	22	3.0	730	10	US-09-741-149-2
5	22	3.0	730	10	US-09-795-693-5
6	15	2.1	676	9	US-09-815-923-12
7	14	1.9	599	10	US-09-861-846-4
8	14	1.9	610	10	US-09-861-846-2
9	11	1.5	579	9	US-09-738-626-4648
10	10	1.4	624	9	US-10-156-239-24
11	10	1.4	624	10	US-09-795-693-24
12	8	1.1	224	10	US-09-843-598-6
13	8	1.1	270	10	US-09-925-302-677
14	8	1.1	421	10	US-09-843-598-9
15	8	1.1	587	9	US-09-815-923-4
16	8	1.1	624	9	US-10-105-959-4
17	8	1.1	671	10	US-09-843-598-5
18	8	1.1	671	10	US-09-843-598-7
19	7	1.0	12	9	US-09-817-144-2

20	7	1.0	15	10	US-09-818-656A-21	Sequence 21, Appl
21	7	1.0	52	10	US-09-864-761-43363	Sequence 43363, A
22	7	1.0	67	10	US-09-864-761-47143	Sequence 47143, A
23	7	1.0	68	10	US-09-864-761-34614	Sequence 34614, A
24	7	1.0	73	9	US-09-796-692-1130	Sequence 1130, Ap
25	7	1.0	102	10	US-09-921-397-31	Sequence 31, Appl
26	7	1.0	112	10	US-09-919-473-10	Sequence 10, Appl
27	7	1.0	127	10	US-09-921-397-110	Sequence 110, App
28	7	1.0	136	9	US-09-764-868-710	Sequence 710, App
29	7	1.0	209	9	US-09-957-187-79	Sequence 79, Appl
30	7	1.0	260	10	US-09-921-397-109	Sequence 109, App
31	7	1.0	266	9	US-09-738-626-6457	Sequence 6457, Ap
32	7	1.0	270	9	US-09-796-753-126	Sequence 126, App
33	7	1.0	270	9	US-09-905-674-2	Sequence 2, Appli
34	7	1.0	270	9	US-09-957-187-16	Sequence 16, Appl
35	7	1.0	297	9	US-09-510-332-87	Sequence 87, Appl
36	7	1.0	300	10	US-09-921-397-107	Sequence 107, App
37	7	1.0	305	9	US-09-510-332-135	Sequence 135, App
38	7	1.0	314	9	US-09-510-332-44	Sequence 44, Appl
39	7	1.0	314	9	US-09-510-332-71	Sequence 71, Appl
40	7	1.0	315	10	US-09-881-752A-54	Sequence 54, Appl
41	7	1.0	319	10	US-09-886-055-95	Sequence 95, Appl
42	7	1.0	335	10	US-09-862-810-4	Sequence 4, Appli
43	7	1.0	348	10	US-09-731-872-247	Sequence 247, App
44	7	1.0	352	9	US-10-102-806-543	Sequence 543, App
45	7	1.0	361	9	US-09-989-442-126	Sequence 126, App

ALIGNMENTS

RESULT 1
US-09-923-444A-2
: Sequence 2, Application US/09923444A
: Patent No. US20020015980A1
: GENERAL INFORMATION:
: APPLICANT: LI, YI
: FLEISCHMANN, ROBERT
: TITLE OF INVENTION: NEUROTRANSMITTER TRANSPORTER
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Human Genome Sciences, Inc.
: STREET: 9410 Key West Avenue
: CITY: Rockville
: STATE: MD
: COUNTRY: US
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/923,444A
: FILING DATE: 08-Aug-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/062,815
: FILING DATE: 199-12-20
: ATTORNEY/AGENT INFORMATION:
: NAME: Michele M. Wales
: REGISTRATION NUMBER: 43,975
: REFERENCE/DOCKET NUMBER: PF116
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8439
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 727 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-923-444A-2

Query Match 100.0%; Score 727; DB 10; Length 727;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 727; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPKNSKVTQREHSHVETESVADLLALBEPVDYKQSVLNAGEAGGKQKAVEEELDAEDR 60
DB 1 MPKNSKVTQREHSHVETESVADLLALBEPVDYKQSVLNAGEAGGKQKAVEEELDAEDR 60

QY 61 PAWSKIQYILAQIGFSGVLGNIRFPYLCOKNGGAVLPVLLVLIIGIIPFLFELEAV 120
DB 61 PAWSKIQYILAQIGFSGVLGNIRFPYLCOKNGGAVLPVLLVLIIGIIPFLFELEAV 120

QY 121 QORTRRSGIGVHHVYICPRLGIGFSSICVCLFVGLYVNIIGWSIFYFFKSFQYPLPWSE 180
DB 121 QORTRRSGIGVHHVYICPRLGIGFSSICVCLFVGLYVNIIGWSIFYFFKSFQYPLPWSE 180

QY 181 CPVVRNGSVAVVEACEKSSATTFWYREALDIDSISESGLNKWKMTLCLLVVWSIGGM 240
DB 181 CPVVRNGSVAVVEACEKSSATTFWYREALDIDSISESGLNKWKMTLCLLVVWSIGGM 240

QY 241 AVGGIOSSGKVMYFSSLPYVVLACFLVRLGLLRGAVDGLHMFPTPKLVKMLDPQVWRE 300
DB 241 AVGGIOSSGKVMYFSSLPYVVLACFLVRLGLLRGAVDGLHMFPTPKLVKMLDPQVWRE 300

QY 301 VATQVFGLGFGGVIIVFSSYNKQDNCHFDGALVSFINFTSVLATLVVVFVVLGFKAN 360
DB 301 VATQVFGLGFGGVIIVFSSYNKQDNCHFDGALVSFINFTSVLATLVVVFVVLGFKAN 360

QY 361 IMNEKCVVNAEKILGYINTNVLSDRLIPPHVNFSLTTKDYMEMDNVIMTVKEDQFSAL 420
DB 361 IMNEKCVVNAEKILGYINTNVLSDRLIPPHVNFSLTTKDYMEMDNVIMTVKEDQFSAL 420

QY 421 GLDPCLEDELDSVQGTGLAFTAMTHFTSPFWSVMFFLMLNLGLGSMIGTMAG 480
DB 421 GLDPCLEDELDSVQGTGLAFTAMTHFTSPFWSVMFFLMLNLGLGSMIGTMAG 480

QY 481 ITTPIIDTSKVPKEMTVGCCVTFELVGLLFVQSRGNYFVTMFDDYSATLPLTLIVILEN 540
DB 481 ITTPIIDTSKVPKEMTVGCCVTFELVGLLFVQSRGNYFVTMFDDYSATLPLTLIVILEN 540

QY 541 IAVAWIYGPKKMQEITMLGFRPYRYFYMKFVSPCLMAVLTTASIIQLGVTTPPAYSA 600
DB 541 IAVAWIYGPKKMQEITMLGFRPYRYFYMKFVSPCLMAVLTTASIIQLGVTTPPAYSA 600

QY 601 WKEEAARYLYFPNPMALLITLIVVATLPIPVFVLRHFLHLLSDGNTLSVSKKARM 660
DB 601 WKEEAARYLYFPNPMALLITLIVVATLPIPVFVLRHFLHLLSDGNTLSVSKKARM 660

QY 661 MKDISNLEENDETRFSLSKVPSAPSPMPTHRSYLPGGSTSPLETSMNPNPGRGYLLA 720
DB 661 MKDISNLEENDETRFSLSKVPSAPSPMPTHRSYLPGGSTSPLETSMNPNPGRGYLLA 720

QY 721 STPESEL 727
DB 721 STPESEL 727

RESULT 2

US-09-741-149-4
; Sequence 4, Application US/09741149
; Patent No. US20020031800A1
; GENERAL INFORMATION:
; APPLICANT: LI, Zhenya et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000780
; CURRENT APPLICATION NUMBER: US/09/741.149
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-741-149-4

Query Match 3.0%; Score 22; DB 10; Length 729;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 FVQSRGNYFVTMFDDYSATLPL 532
DB 512 FVQSRGNYFVTMFDDYSATLPL 533

RESULT 3

US-10-156-239-5
; Sequence 5, Application US/10156239
; Publication No. US20030036074A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: No. US20030036074A1 Nucleic Acid Sequences Encoding Human T
; TITLE OF INVENTION: ATPase Molecule, A Human Ubiquitin Conjugating Enzyme-Like Molecule,
; TITLE OF INVENTION: Ubiquitin Conjugating Enzyme-Like Molecule, and Uses Thereof
; FILE REFERENCE: 35800/247645
; CURRENT APPLICATION NUMBER: US/10/156,239
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 09/795,693
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/809,557
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/192,018
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/808,568
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/191,790
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/808,767
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/191,781
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-156-239-5

Query Match 3.0%; Score 22; DB 9; Length 730;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 FVQSRGNYFVTMFDDYSATLPL 532
DB 512 FVQSRGNYFVTMFDDYSATLPL 533

RESULT 4

US-09-741-149-2
; Sequence 2, Application US/09741149
; Patent No. US20020031800A1
; GENERAL INFORMATION:
; APPLICANT: LI, Zhenya et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000780
; CURRENT APPLICATION NUMBER: US/09/741.149
; CURRENT FILING DATE: 2000-12-21

; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Human
US-09-741-149-2

Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-12; Length 730;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 FVQRSGNYFVTMDDYSATLPL 532
Db 512 FVQRSGNYFVTMDDYSATLPL 533

RESULT 5
US-09-795-693-5
; Sequence 5, Application US/09795693
; Patent No. US20020068710A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
; TITLE OF INVENTION: 32613, No. US20020068710A1el Human Transporters
; FILE REFERENCE: 35800/209292
; CURRENT APPLICATION NUMBER: US/09/795,693
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-693-5

Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-12; Length 730;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 FVQRSGNYFVTMDDYSATLPL 532
Db 512 FVQRSGNYFVTMDDYSATLPL 533

RESULT 6
US-09-815-923-12
; Sequence 12, Application US/09815923
; Publication No. US20020197644A1
; GENERAL INFORMATION:
; APPLICANT: Gill, Sarjeet S.
; APPLICANT: Ross, Linda S.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. US20020197644A1el
; TITLE OF INVENTION: Target Sites for Insecticides
; FILE REFERENCE: 023070-093800US
; CURRENT APPLICATION NUMBER: US/09/815,923
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Manduca sexta
; FEATURE:
; OTHER INFORMATION: orphan transporter
US-09-815-923-12

Query Match
Best Local Similarity 100.0%; Pred. No. 7.5e-06; Length 676;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 SVGLGNIWRFPYLCQ 91
Db 69 SVGLGNIWRFPYLCQ 83

RESULT 7
US-09-861-846-4
; Sequence 4, Application US/09861846
; Patent No. US20020110852A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001065
; CURRENT APPLICATION NUMBER: US/09/861,846
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/752,821
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-861-846-4

Query Match
Best Local Similarity 100.0%; Pred. No. 6.2e-05; Length 599;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 VGLGNIWRFPYLCQ 91
Db 35 VGLGNIWRFPYLCQ 48

RESULT 8
US-09-861-846-2
; Sequence 2, Application US/09861846
; Patent No. US20020110852A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001065
; CURRENT APPLICATION NUMBER: US/09/861,846
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/752,821
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Human
US-09-861-846-2

Query Match
Best Local Similarity 100.0%; Pred. No. 6.3e-05; Length 610;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 VGLGNIWRFPYLCQ 91
Db 36 VGLGNIWRFPYLCQ 49

RESULT 9
US-09-738-626-4648
; Sequence 4648, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patent in ver. 3.0
SEQ ID NO 4648
LENGTH: 579
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-4648

Query Match 1.5%; Score 11; DB 9; Length 579;
Best Local Similarity 100.0%; Pred. No. 0.047; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0

QY 78 VGLGNWRFPY 88
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DB 52 VGLGNWRFPY 62

RESULT 10
US-10-156-239-24
Sequence 24, Application US/10156239
Publication No. US20030036074A1
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: NO. US20030036074A1el Nucleic Acid Sequences Encoding Human Trans
TITLE OF INVENTION: ATPase Molecule, A Human Ubiquitin Hydrolase-Like Molecule, A Hu
TITLE OF INVENTION: Ubiquitin Conjugating Enzyme-Like Molecule, and Uses Therefor
FILE REFERENCE: 35800/247645
CURRENT APPLICATION NUMBER: US/10/156,239
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 09/795,693
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/185,906
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/809,557
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 60/192,018
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 09/808,568
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/191,790
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 09/808,767
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 60/191,791
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 624
TYPE: PRT
ORGANISM: Artificial Sequence

OTHER INFORMATION: Pfam consensus sequence
US-10-156-239-24

Query Match 1.4%; Score 10; DB 9; Length 624;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 GIPLFFLELA 119
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DB 51 GIPLFFLELA 60

RESULT 11
US-09-795-693-24
Sequence 24, Application US/09795693
Patent No. US20020068710A1
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
FILE REFERENCE: 32613, No. US20020068710A1el Human Transporters
CURRENT APPLICATION NUMBER: US/09/795,693
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/185,906
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 624
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Pfam consensus sequence
US-09-795-693-24

Query Match 1.4%; Score 10; DB 10; Length 624;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 GIPLFFLELA 119
|||||
DB 51 GIPLFFLELA 60

RESULT 12
US-09-843-598-6
Sequence 6, Application US/09843598
Patent No. US20020010944A1
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Ranganathan, Rajesh
TITLE OF INVENTION: CESERT GENES, PROTEINS, AND MODULATORY
TITLE OF INVENTION: COMPOUNDS
FILE REFERENCE: 01997/525002
CURRENT APPLICATION NUMBER: US/09/843,598
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/200,549
PRIOR FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 224
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-843-598-6

Query Match 1.1%; Score 8; DB 10; Length 224;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 LGNIWRFP 87
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DB 120 LGNIWRFP 127

RESULT 13

US-09-925-302-677
; Sequence 677, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 677
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-677

Query Match 1.1%; Score 8; DB 10; Length 270;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 476 GTMAGITT 483
|||||||
Db 21 GTMAGITT 28

RESULT 14

US-09-843-598-9
; Sequence 9, Application US/09843598
; Patent No. US20020010944A1
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Ranganathan, Rajesh
; TITLE OF INVENTION: CSEFT GENES, PROTEINS, AND MODULATORY
; TITLE OF INVENTION: COMPOUNDS
; FILE REFERENCE: 01997/525002
; CURRENT APPLICATION NUMBER: US/09/843,598
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/200,549
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-843-598-9

Query Match 1.1%; Score 8; DB 10; Length 421;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 LGNIWRFP 87
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Db 120 LGNIWRFP 127

RESULT 15

US-09-815-923-4
; Sequence 4, Application US/09815923
; Publication No. US20020197644A1
; GENERAL INFORMATION:
; APPLICANT: Gill, Sarjeet S.
; APPLICANT: Ross, Linda S.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. US20020197644A1

; TITLE OF INVENTION: Target Sites for Insecticides
; FILE REFERENCE: 023070-033800US
; CURRENT APPLICATION NUMBER: US/09/815,923
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 587
; TYPE: PRT
; ORGANISM: Manduca sexta
; FEATURE:
; OTHER INFORMATION: serotonin transporter
US-09-815-923-4

Query Match 1.1%; Score 8; DB 9; Length 587;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 112 PLFFELEA 119
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Db 90 PLFFELEA 97

Search completed: April 21, 2003, 14:19:57
Job time : 45 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 14:09:29 ; Search time 18 Seconds
(without alignments)
1188.359 Million cell updates/sec

Title: US-09-923-444A-2

Perfect score: 727
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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0
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Post-processing: listing first 45 summaries

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Issued Patents, AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	540	74.3	727	1 US-08-424-424B-2	Sequence 2, Appli
2	540	74.3	727	5 PCT-US94-05365A-2	Sequence 2, Appli
3	11	1.5	247	4 US-09-134-001C-2877	Sequence 2, Appli
4	9	1.2	607	1 US-07-959-943-7	Sequence 7, Appli
5	9	1.2	607	1 US-07-879-617A-12	Sequence 12, Appli
6	9	1.2	607	1 US-08-753-985-12	Sequence 12, Appli
7	9	1.2	607	1 US-08-149-100-2	Sequence 2, Appli
8	9	1.2	607	1 US-07-559-943-9	Sequence 9, Appli
9	9	1.2	635	1 US-07-879-617A-9	Sequence 9, Appli
10	9	1.2	635	1 US-08-753-985-9	Sequence 9, Appli
11	9	1.2	653	1 US-07-782-298-2	Sequence 2, Appli
12	9	1.2	667	1 US-07-879-617A-8	Sequence 8, Appli
13	9	1.2	667	1 US-08-753-985-8	Sequence 8, Appli
14	8	1.1	1278	4 US-09-462-136-2	Sequence 2, Appli
15	8	1.1	8	4 US-08-444-818-671	Sequence 671, App
16	7	1.0	11	1 US-08-707-873-1	Sequence 1, Appli
17	7	1.0	11	2 US-08-707-874-1	Sequence 1, Appli
18	7	1.0	11	2 US-08-315-067-1	Sequence 1, Appli
19	7	1.0	11	3 US-09-193-797-1	Sequence 1, Appli
20	7	1.0	11	5 PCT-US95-01770-1	Sequence 1, Appli
21	7	1.0	12	4 US-09-146-755-2	Sequence 2, Appli
22	7	1.0	20	2 US-07-894-063A-28	Sequence 28, Appli
23	7	1.0	86	4 US-09-134-001C-3928	Sequence 3928, Ap
24	7	1.0	152	4 US-08-444-818-62	Sequence 62, Appli
25	7	1.0	187	1 US-07-853-985A-2	Sequence 2, Appli
26	7	1.0	187	1 US-07-681-703B-2	Sequence 2, Appli
27	7	1.0	187	1 US-08-184-236-2	Sequence 2, Appli

28	7	1.0	187	2 US-08-407-410B-2	Sequence 2, Appli
29	7	1.0	187	2 US-08-485-500-2	Sequence 2, Appli
30	7	1.0	187	5 PCT-US91-02370-2	Sequence 2, Appli
31	7	1.0	187	5 PCT-US94-04174-2	Sequence 2, Appli
32	7	1.0	244	4 US-09-134-001C-4735	Sequence 4735, Ap
33	7	1.0	262	4 US-09-134-001C-5418	Sequence 5418, Ap
34	7	1.0	273	4 US-09-134-001C-3016	Sequence 3016, Ap
35	7	1.0	305	1 US-08-266-451B-26	Sequence 26, Appli
36	7	1.0	305	2 US-08-748-725-26	Sequence 26, Appli
37	7	1.0	312	1 US-08-240-783B-6	Sequence 6, Appli
38	7	1.0	312	3 US-09-084-813-6	Sequence 6, Appli
39	7	1.0	312	5 PCT-US92-09662-6	Sequence 30, Appli
40	7	1.0	361	3 US-09-028-934-30	Sequence 12, Appli
41	7	1.0	387	4 US-08-867-611-12	Sequence 17, Appli
42	7	1.0	387	5 PCT-US92-06965A-17	Sequence 4, Appli
43	7	1.0	410	4 US-08-725-758A-4	Sequence 3805, Ap
44	7	1.0	420	4 US-09-134-001C-3805	Sequence 2, Appli
45	7	1.0	426	4 US-08-725-758A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-424-424B-2
; Sequence 2, Application US/08424424B
; Patent No. 5759854
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Neurotransmitter Transporter
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,424B
FILING DATE: APRIL 21, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05363
FILING DATE: MAY 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 727 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-424-424B-2

Query Match 74.3%; Score 540; DB 1; Length 727;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
188 SAAYAEAEKSSATYFEYREALDISISSEGLNWKMTCLLYVSIQMAVGKGIQ 247
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Db 188 SVAVVEAECEKSSATTFYFWYREALDISDSISESGGLNMKMTLLCLLVWSIGMAVGKGIQ 247
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Db 248 SSGKVMFESSLPYVYLACFLVRLGILLRGAVDGLIHMFPTKLVKMLDPQVREVAQVFE 307
QY 308 GGLGFGGIVFSSYNKQDNCHFDGALVSFINFTSVLATLVFVVLGFKANINNEKCV 367
Db 308 GGLGFGGIVFSSYNKQDNCHFDGALVSFINFTSVLATLVFVVLGFKANINNEKCV 367
QY 368 VENAERILGYLNTNVLSDRLIPPHVNSHLTKDYMEMDNVIMTVKEDQFSALGDPCLL 427
Db 368 VENAERILGYLNTNVLSDRLIPPHVNSHLTKDYMEMDNVIMTVKEDQFSALGDPCLL 427
QY 428 EDELKSVQGTGLAFIAFTEAMTHPTSPFWSVMEFLMLINLGSGMIGTAGITPPIID 487
Db 428 EDELKSVQGTGLAFIAFTEAMTHPTSPFWSVMEFLMLINLGSGMIGTAGITPPIID 487
QY 488 TSXVPEKEMFTVGCCTFELVGLLFVQSRGNYFVTMEDYSATLPLLLIENIAVAMIY 547
Db 488 TSXVPEKEMFTVGCCTFELVGLLFVQSRGNYFVTMEDYSATLPLLLIENIAVAMIY 547
QY 548 GPKKFMQELTEMLGFRPRFYFYMKKFSVPLCMAVLTTASTIOLGVTTPAYSAWIKKEEA 607
Db 548 GPKKFMQELTEMLGFRPRFYFYMKKFSVPLCMAVLTTASTIOLGVTTPAYSAWIKKEEA 607
QY 608 ERYLYFPNMPALLITLIVATLPIPVYFVLRHFLHLSGNSNTLSVSKKARMMKDISNL 667
Db 608 ERYLYFPNMPALLITLIVATLPIPVYFVLRHFLHLSGNSNTLSVSKKARMMKDISNL 667
QY 668 EENDETRFLSKVSEAPSPMPTHRSYLGPSTSPLETSMNNGPYGRGYLLASTPESEL 727
Db 668 EENDETRFLSKVSEAPSPMPTHRSYLGPSTSPLETSMNNGPYGRGYLLASTPESEL 727

RESULT 2
PCT-US94-05363A-2
; Sequence 2, Application PC/TUS9405363A
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Neurotransmitter Transporter
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILLILLAN,
; ADDRESS: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05363A
; FILING DATE: SUBMITTED HEREMITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 AMINO ACIDS
; TYPE: AMINO ACID

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; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; PCT-US94-05363A-2
Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 SVAVVEAECEKSSATTFYFWYREALDISDSISESGGLNMKMTLLCLLVWSIGMAVGKGIQ 247
Db 188 SVAVVEAECEKSSATTFYFWYREALDISDSISESGGLNMKMTLLCLLVWSIGMAVGKGIQ 247
QY 248 SSGKVMFESSLPYVYLACFLVRLGILLRGAVDGLIHMFPTKLVKMLDPQVREVAQVFE 307
Db 248 SSGKVMFESSLPYVYLACFLVRLGILLRGAVDGLIHMFPTKLVKMLDPQVREVAQVFE 307
QY 308 GGLGFGGIVFSSYNKQDNCHFDGALVSFINFTSVLATLVFVVLGFKANINNEKCV 367
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QY 368 VENAERILGYLNTNVLSDRLIPPHVNSHLTKDYMEMDNVIMTVKEDQFSALGDPCLL 427
Db 368 VENAERILGYLNTNVLSDRLIPPHVNSHLTKDYMEMDNVIMTVKEDQFSALGDPCLL 427
QY 428 EDELKSVQGTGLAFIAFTEAMTHPTSPFWSVMEFLMLINLGSGMIGTAGITPPIID 487
Db 428 EDELKSVQGTGLAFIAFTEAMTHPTSPFWSVMEFLMLINLGSGMIGTAGITPPIID 487
QY 488 TSXVPEKEMFTVGCCTFELVGLLFVQSRGNYFVTMEDYSATLPLLLIENIAVAMIY 547
Db 488 TSXVPEKEMFTVGCCTFELVGLLFVQSRGNYFVTMEDYSATLPLLLIENIAVAMIY 547
QY 548 GPKKFMQELTEMLGFRPRFYFYMKKFSVPLCMAVLTTASTIOLGVTTPAYSAWIKKEEA 607
Db 548 GPKKFMQELTEMLGFRPRFYFYMKKFSVPLCMAVLTTASTIOLGVTTPAYSAWIKKEEA 607
QY 608 ERYLYFPNMPALLITLIVATLPIPVYFVLRHFLHLSGNSNTLSVSKKARMMKDISNL 667
Db 608 ERYLYFPNMPALLITLIVATLPIPVYFVLRHFLHLSGNSNTLSVSKKARMMKDISNL 667
QY 668 EENDETRFLSKVSEAPSPMPTHRSYLGPSTSPLETSMNNGPYGRGYLLASTPESEL 727
Db 668 EENDETRFLSKVSEAPSPMPTHRSYLGPSTSPLETSMNNGPYGRGYLLASTPESEL 727

RESULT 3
US-09-134-001C-2877
; Sequence 2877, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2877
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2877

Query Match
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 VGLGNITWRFPY 88

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,985
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/879617
FILING DATE: 01-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMU109
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6508
TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 607 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rattus
TISSUE TYPE: Brain - serotonin transporter
FEATURE:
NAME/KEY: Active-site
LOCATION: 95..96
OTHER INFORMATION: /note= "Leucine zipper motif"
FEATURE:
NAME/KEY: Active-site
LOCATION: 102..103
OTHER INFORMATION: /note= "Leucine zipper motif"
FEATURE:
NAME/KEY: Active-site
LOCATION: 109..110
OTHER INFORMATION: /note= "Leucine zipper motif"
FEATURE:
NAME/KEY: Active-site
LOCATION: 116..117
OTHER INFORMATION: /note= "Leucine zipper motif"
US-08-753-985-12

Query Match 1.2%; Score 9; DB 1; Length 607;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 LGNIWRFPY 88
Db 76 LGNIWRFPY 84

RESULT 7
US-08-149-100-2
Sequence 2, Application US/08149100
Patent No. 5559021
GENERAL INFORMATION:
APPLICANT: Smith, Kelli E.
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING A NOVEL MAMMALIAN
TRANSPORTER HOMOLOGOUS TO NEUROTRANSMITTER TRANSPORTERS
TITLE OF INVENTION: TRANSPORTER HOMOLOGOUS TO NEUROTRANSMITTER TRANSPORTERS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF INVENTIONS: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,100
FILING DATE: 08-NOV-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44744/JPW/TEP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 6640525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 616 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-149-100-2

Query Match 1.2%; Score 9; DB 1; Length 616;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 435 VOGTGLAFI 443
Db 392 VOGTGLAFI 400

RESULT 8
US-07-959-943-9
Sequence 9, Application US/07959943
Patent No. 5418162
GENERAL INFORMATION:
APPLICANT: Blakely, Randy D.
APPLICANT: Freneau Jr., Robert T.
APPLICANT: Caron, Marc G.
TITLE OF INVENTION: Serotonin Transporter cDNA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park
ADDRESSEE: and
ADDRESSEE: Gibson
STREET: Post Office Drawer 31107
CITY: Raleigh
STATE: No. 5418162th Carolina
COUNTRY: U.S.A.
ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,943
FILING DATE: 19921014
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405.38a
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175

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Db 55 VGLNIWRFPY 65
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RESULT 4
US-07-959-943-7
; Sequence 7, Application US/07959943
; Patent No. 5418162
; GENERAL INFORMATION:
; APPLICANT: Blakely, Randy D.
; APPLICANT: Fremereau Jr., Robert T.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Serotonin Transporter cDNA
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park
; ADDRESSEE: and
; ADDRESSEE: Gibson
; STREET: Post Office Drawer 31107
; CITY: Raleigh
; STATE: No. 5418162th Carolina
; COUNTRY: U.S.A.
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,943
; FILING DATE: 19921014
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5405.38a
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 607 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-959-943-7

Query Match 1.2%; Score 9; DB 1; Length 607;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 LGNIWRFPY 88
|||||
Db 76 LGNIWRFPY 84

RESULT 5
US-07-879-617A-12
; Sequence 12, Application US/07879617A
; Patent No. 5580775
; GENERAL INFORMATION:
; APPLICANT: Fremereau Jr., Robert T.
; APPLICANT: Caron, Marc G.
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: A High Affinity L-Proline Transporter
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30309

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,617A
; FILING DATE: 19920501
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: EMU109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-815-6508
; TELEFAX: 404-815-6555
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 607 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rattus
; TISSUE TYPE: Brain - serotonin transporter
; FEATURE:
; NAME/KEY: Active-site
; LOCATION: 95..96
; OTHER INFORMATION: /note= "Leucine zipper motif"
; FEATURE:
; NAME/KEY: Active-site
; LOCATION: 102..103
; OTHER INFORMATION: /note= "Leucine zipper motif"
; FEATURE:
; NAME/KEY: Active-site
; LOCATION: 109..110
; OTHER INFORMATION: /note= "Leucine zipper motif"
; FEATURE:
; NAME/KEY: Active-site
; LOCATION: 116..117
; OTHER INFORMATION: /note= "Leucine zipper motif"
; US-07-879-617A-12

Query Match 1.2%; Score 9; DB 1; Length 607;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 LGNIWRFPY 88
|||||
Db 76 LGNIWRFPY 84

RESULT 6
US-08-753-985-12
; Sequence 12, Application US/08753985
; Patent No. 5759788
; GENERAL INFORMATION:
; APPLICANT: Fremereau Jr., Robert T.
; APPLICANT: Caron, Marc G.
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: A High Affinity L-Proline Transporter
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30309
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 630 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-959-943-9

Query Match 1.2%; Score 9; DB 1; Length 630;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 LGNIWRFPY 88
IIIIIIIIII
DB 99 LGNIWRFPY 107

RESULT 9
US-07-879-617A-9
Sequence 9, Application US/07879617A
Patent No. 5580775
GENERAL INFORMATION:
APPLICANT: Freneau Jr., Robert T.
APPLICANT: Caron, Marc G.
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: A High Affinity L-Proline Transporter
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879, 617A
FILING DATE: 19920501
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMU109
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6508
TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 635 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rattus
TISSUE TYPE: Brain - Proline Transporter
FEATURE:
NAME/KEY: Domain
LOCATION: 46..65
OTHER INFORMATION: /note= "Proposed transmembrane domain."
OTHER INFORMATION: domain.
FEATURE:
NAME/KEY: Domain
LOCATION: 72..97
OTHER INFORMATION: /note= "Proposed transmembrane domain."
OTHER INFORMATION: domain.

FEATURE:
NAME/KEY: Domain
LOCATION: 117..137
OTHER INFORMATION: /note= "Proposed transmembrane domain."
OTHER INFORMATION: domain.
FEATURE:
NAME/KEY: Domain
LOCATION: 217..236
OTHER INFORMATION: /note= "Proposed transmembrane domain."
OTHER INFORMATION: domain.
FEATURE:
NAME/KEY: Domain
LOCATION: 243..264
OTHER INFORMATION: /note= "Proposed transmembrane domain."
OTHER INFORMATION: domain.
FEATURE:
NAME/KEY: Domain
LOCATION: 291..311
OTHER INFORMATION: /note= "Proposed transmembrane domain."
OTHER INFORMATION: domain.
FEATURE:
NAME/KEY: Domain
LOCATION: 322..345
OTHER INFORMATION: /note= "Proposed transmembrane domain."
OTHER INFORMATION: domain.
FEATURE:
NAME/KEY: Domain
LOCATION: 373..397
OTHER INFORMATION: /note= "Proposed transmembrane domain."
OTHER INFORMATION: domain.
FEATURE:
NAME/KEY: Domain
LOCATION: 424..443
OTHER INFORMATION: /note= "Proposed transmembrane domain."
OTHER INFORMATION: domain.
FEATURE:
NAME/KEY: Domain
LOCATION: 456..479
OTHER INFORMATION: /note= "Proposed transmembrane domain."
OTHER INFORMATION: domain.
FEATURE:
NAME/KEY: Domain
LOCATION: 500..519
OTHER INFORMATION: /note= "Proposed transmembrane domain."
OTHER INFORMATION: domain.
FEATURE:
NAME/KEY: Domain
LOCATION: 536..559
OTHER INFORMATION: /note= "Proposed transmembrane domain."
OTHER INFORMATION: domain.
FEATURE:
NAME/KEY: Active-site
LOCATION: 76..77
OTHER INFORMATION: /note= "Leucine zipper motif"
OTHER INFORMATION: domain.
FEATURE:
NAME/KEY: Active-site
LOCATION: 83..84
OTHER INFORMATION: /note= "Leucine zipper motif"
OTHER INFORMATION: domain.
FEATURE:
NAME/KEY: Active-site
LOCATION: 90..91
OTHER INFORMATION: /note= "Leucine zipper motif"
OTHER INFORMATION: domain.
FEATURE:
NAME/KEY: Active-site
LOCATION: 97..98
OTHER INFORMATION: /note= "Leucine zipper motif"
OTHER INFORMATION: domain.
US-07-879-617A-9

Query Match 1.2%; Score 9; DB 1; Length 635;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 GIPLFLEL 118

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Db      87  G1PLFFLEL 95
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RESULT 10
US-08-753-985-9
; Sequence 9, Application US/08753985
; Patent No. 5759788
; GENERAL INFORMATION:
; APPLICANT: Frembeau Jr., Robert T.
; APPLICANT: Caron, Marc G.
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: A High Affinity L-Proline Transporter
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/753,985
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/879617
; FILING DATE: 01-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Padst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: EMU109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-815-6508
; TELEFAX: 404-815-6555
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rattus
; TISSUE TYPE: Brain - Proline Transporter
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 46..65
; OTHER INFORMATION: /note= "Proposed transmembrane
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 72..97
; OTHER INFORMATION: /note= "Proposed transmembrane
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 117..137
; OTHER INFORMATION: /note= "Proposed transmembrane
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 217..236
; OTHER INFORMATION: /note= "Proposed transmembrane
; OTHER INFORMATION: domain."

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; FEATURE:
; NAME/KEY: Domain
; LOCATION: 243..264
; OTHER INFORMATION: /note= "Proposed transmembrane
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 291..311
; OTHER INFORMATION: /note= "Proposed transmembrane
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 322..345
; OTHER INFORMATION: /note= "Proposed transmembrane
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 373..397
; OTHER INFORMATION: /note= "Proposed transmembrane
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 424..443
; OTHER INFORMATION: /note= "Proposed transmembrane
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 456..479
; OTHER INFORMATION: /note= "Proposed transmembrane
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 500..519
; OTHER INFORMATION: /note= "Proposed transmembrane
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 536..559
; OTHER INFORMATION: /note= "Proposed transmembrane
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Active-site
; LOCATION: 76..77
; OTHER INFORMATION: /note= "Leucine zipper motif"
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Active-site
; LOCATION: 83..84
; OTHER INFORMATION: /note= "Leucine zipper motif"
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Active-site
; LOCATION: 90..91
; OTHER INFORMATION: /note= "Leucine zipper motif"
; OTHER INFORMATION: domain."
; FEATURE:
; NAME/KEY: Active-site
; LOCATION: 97..98
; OTHER INFORMATION: /note= "Leucine zipper motif"
; OTHER INFORMATION: domain."
;
; US-08-753-985-9
;
; Query Match 1.2%; Score 9; DB 1; Length 635;
; Best Local Similarity 100.0%; Pred. No. 2.3;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 110 G1PLFFLEL 118
;      |||||||
; Db 87 G1PLFFLEL 95
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; RESULT 11
; US-07-782-298-2
; Sequence 2, Application US/07782298
; Patent No. 5552308
; GENERAL INFORMATION:
; APPLICANT: Hoffman, Beth J.
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; APPLICANT: Mezey, Eva
; APPLICANT: Brownstein, Michael J.
; TITLE OF INVENTION: cDNA Clone of a Rat Serotonin
; TITLE OF INVENTION: Transporter and Protein Encoded Thereby
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/782,298
; FILING DATE: October 24, 1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerald M. Murphy, Jr.
; REGISTRATION NUMBER: 28,977
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-782-298-2

Query Match 1.2%; Score 9; DB 1; Length 653;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 80 LGNIWRFY 88
DB 99 LGNIWRFY 107

RESULT 12
US-07-879-617A-8
; Sequence 8, Application US/07879617A
; Patent No. 5580775
; GENERAL INFORMATION:
; APPLICANT: Frembeau Jr., Robert T.
; APPLICANT: Caron, Marc G.
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: A High Affinity L-Proline Transporter
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,617A
; FILING DATE: 19920501
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: EMU109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-815-6508
; TELEFAX: 404-815-6555
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 667 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rattus
; TISSUE TYPE: Brain
; IMMEDIATE SOURCE:
; LIBRARY: rat forebrain cDNA library
; CLONE: rTB2-2-20
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 76..95
; OTHER INFORMATION: /note= "Membrane-spanning domain"
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 103..127
; OTHER INFORMATION: /note= "Membrane-spanning domain"
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 147..167
; OTHER INFORMATION: /note= "Membrane-spanning domain"
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 247..266
; OTHER INFORMATION: /note= "Membrane-spanning domain"
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 272..294
; OTHER INFORMATION: /note= "Membrane-spanning domain"
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 321..341
; OTHER INFORMATION: /note= "Membrane-spanning domain"
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 353..375
; OTHER INFORMATION: /note= "Membrane-spanning domain"
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 404..427
; OTHER INFORMATION: /note= "Membrane-spanning domain"
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 454..473
; OTHER INFORMATION: /note= "Membrane-spanning domain"
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 487..509
; OTHER INFORMATION: /note= "Membrane-spanning domain"
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 530..549
; OTHER INFORMATION: /note= "Membrane-spanning domain"
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 567..589
; OTHER INFORMATION: /note= "Membrane-spanning domain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 44..45
; OTHER INFORMATION: /note= "protein kinase C phosphorylation site"
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NAME/KEY: Region
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NAME/KEY: Region
LOCATION: 269..270
OTHER INFORMATION: /note= "protein kinase C phosphorylation site"
FEATURE:
NAME/KEY: Region
LOCATION: 630..631
OTHER INFORMATION: /note= "protein kinase C phosphorylation site"
FEATURE:
NAME/KEY: Region
LOCATION: 106..127
OTHER INFORMATION: /note= "Leucine zipper motif"
FEATURE:
NAME/KEY: Region
LOCATION: 212..213
OTHER INFORMATION: /note= "N-linked glycosylation site"
US-07-879-617A-8
Query Match 1.2%; Score 9; DB 1; Length 667;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 GIPFLFLEL 118
Db 117 GIPFLFLEL 125

RESULT 13
US-08-753-985-8
Sequence 8, Application US/08753985
Patent No. 5759788
GENERAL INFORMATION:
APPLICANT: Freneau Jr., Robert T.
APPLICANT: Caron, Marc G.
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: A High Affinity L-Proline Transporter
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08753.985
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/879617
FILING DATE: 01-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMU109
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6508
TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

```

```

LENGTH: 667 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rattus
TISSUE TYPE: Brain
IMMEDIATE SOURCE:
LIBRARY: rat forebrain cDNA library
CLONE: rTB2-2-20
FEATURE:
NAME/KEY: Domain
LOCATION: 76..95
OTHER INFORMATION: /note= "Membrane-spanning domain"
FEATURE:
NAME/KEY: Domain
LOCATION: 103..127
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NAME/KEY: Domain
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NAME/KEY: Domain
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FEATURE:
NAME/KEY: Domain
LOCATION: 272..294
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NAME/KEY: Region
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OTHER INFORMATION: /note= "protein kinase C phosphorylation site"
FEATURE:
NAME/KEY: Region
LOCATION: 71..72
OTHER INFORMATION: /note= "cAMP-dependent protein kinase phosphorylation site"
FEATURE:

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NAME/KEY: Region
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LOCATION: 106..127
OTHER INFORMATION: /note= "Leucine zipper motif"
FEATURE:
NAME/KEY: Region
LOCATION: 212..213
OTHER INFORMATION: /note= "N-linked glycosylation site"
OTHER INFORMATION: site"
US-08-753-985-8

Query Match 1.2%; Score 9; DB 1; Length 667;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 GIPFLFLEL 118
|||||
Db 117 GIPFLFLEL 125

RESULT 14

US-09-462-136-2
Sequence 2, Application US/09462136
Patent No. 6426198
GENERAL INFORMATION:
APPLICANT: Carstee, et al.
TITLE OF INVENTION: Genes for Niemann-Pick Type C Disease
FILE REFERENCE: 4239-53894
CURRENT APPLICATION NUMBER: US/09/462.136
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/US98/13862
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/051,682
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1278
TYPE: PRT
ORGANISM: Homo sapiens
US-09-462-136-2

Query Match 1.1%; Score 8; DB 4; Length 1278;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 LPLTLIVI 537
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Db 680 LPLTLIVI 687

RESULT 15

US-08-444-818-671
Sequence 671, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NAMBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville

STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 671:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-818-671

Query Match 1.0%; Score 7; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 444 AFTEAMT 450
|||||
Db 1 AFTEAMT 7

Search completed: April 21, 2003, 14:12:01
Job time : 21 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 14:05:49 ; Search time 41 Seconds
(without alignments)
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Title: US-09-923-444A-2
Perfect score: 727
Sequence: 1 MPKNSKVTQREHSSEHVTE.....NPNPGYGRGYLLASTPESEL 727

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues
Word size : 0
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	626	86.1	727	17	Human HIPHOM 00000
2	182	25.0	727	23	Human NS protein s
3	56	7.7	266	23	Human polypeptide
4	52	7.2	122	22	Human neurotransmi
5	44	6.1	143	22	Rat EST encoded pr
6	37	5.1	127	22	Rat EST encoded pr
7	26	3.6	83	22	Human orphan trans
8	22	3.0	185	22	Human secreted pro
9	22	3.0	188	23	Human secreted pro
10	22	3.0	188	23	Human secreted pro

11	22	3.0	259	23	AAO21214	Sodium-dependent n
12	22	3.0	332	22	AAO64743	Human sodium neuro
13	22	3.0	729	23	AAO21215	Protein sequence i
14	22	3.0	730	22	AAO67159	Amino acid sequenc
15	22	3.0	730	22	AAO72908	Human NTF7 protein
16	22	3.0	730	23	AAO77168	Human GABA transpo
17	22	3.0	730	23	AAO14404	Human neurotransmi
18	19	2.6	249	22	AAO92689	Human protein sequ
19	18	2.5	136	22	ABO11223	Human orphan trans
20	16	2.2	289	22	AAO94304	Human protein sequ
21	15	2.1	675	22	AAO05100	Drosophila melanog
22	15	2.1	744	22	ABO1363	Drosophila melanog
23	14	1.9	259	22	ABO23381	Novel human diago
24	14	1.9	259	22	ABO23431	Novel human diago
25	12	1.7	12	20	AAO32821	Sodium-, chloride-
26	11	1.5	247	23	ABO38032	Staphylococcus epi
27	11	1.5	318	22	AAO57896	Propionibacterium
28	11	1.5	579	22	AAO90894	C. glutamicum prote
29	11	1.5	596	20	AAO9518	C. elegans dopamin
30	11	1.5	615	20	AAO9517	C. elegans dopamin
31	9	1.2	592	23	AAO14408	Human neurotransmi
32	9	1.2	607	14	AAO34662	Rat 5HT transporte
33	9	1.2	607	16	AAO76072	Rat 5HT transporte
34	9	1.2	616	17	AAO7635	Rat brain derived
35	9	1.2	616	22	AAO64193	Human nerve mass-t
36	9	1.2	630	14	AAO34663	Rat 5HT transporte
37	9	1.2	630	16	AAO76073	Rat 5HT transporte
38	9	1.2	637	18	AAO11704	High affinity Na+-
39	9	1.2	647	20	AAO73376	Human HPDVT78 prot
40	9	1.2	653	13	AAO25642	5HT serotonin tra
41	9	1.2	667	19	AAO57224	Rat proline transp
42	8	1.1	101	23	AAO33274	Human transport pr
43	8	1.1	106	22	ABO18975	Novel human diago
44	8	1.1	116	23	ABO89187	Human polypeptide
45	8	1.1	130	20	AAO12151	Human 5' EST secre

ALIGNMENTS

RESULT 1
AAR88390
ID AAR88390 standard; Protein; 727 AA.
XX
AC AAR88390;
XX
DT 15-OCT-1996 (first entry)
XX
DE Human neurotransmitter transporter protein.
XX
KW Neurotransmitter transporter protein; pain therapy; stroke therapy;
amytrophic lateral sclerosis.
XX
OS Homo sapiens.
XX
PN WO9531539-A1.
XX
PD 23-NOV-1995.
XX
PF 16-MAY-1994; 94WO-US05363.
XX
PR 16-MAY-1994; 94WO-US05363.
PR 26-MAY-1994; 94ZA-0003696.
XX
{HUMA-} HUMAN GENOME SCI INC.
XX
PI Fleischmann RD, Li Y;
XX
DR WPI; 1996-010925/01.
XX
N-PSDB; AAT09866.
XX
DNA encoding neuro:transmitter transporter protein and related
(ant)agonists - useful to treat e.g., amytrophic lateral sclerosis,
PT

ABB06153;
10-MAY-2002 (first entry)
Human NS protein sequence SEQ ID NO:245.
Human; cytostatic; osteopathic; gynaecological; neuroprotective;
antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
anorectic; muscular; antinfertility; cardiovascular; anticoagulant;
antibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;
anticonvulsant; antidiabetic; tranquilliser; antidepressant; neuroleptic;
gastrointestinal; virucide; antiulcer; cerebroprotective; nootropic;
contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
endometriosis; degenerative disease; multiple sclerosis; psoriasis;
rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
infertility; cardiovascular disease; coagulation disease; hypertension;
ischemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
gastric ulcer; Alzheimer's disease.
Homo sapiens.
WO200206315-A2.
24-JAN-2002.
17-JUL-2001; 2001WO-IL00653.
18-JUL-2000; 2000IL-0137345.
15-DEC-2000; 2000IL-0140354.
(COMP-) COMPUGEN LTD.
Mintz L, Freilich S, Bernstein J;
WPI; 2002-155037/20.
N-PSDB; ABL39807.
One hundred and twenty eight novel nucleic acid sequences, useful for
treating and diagnosing e.g. cancer, asthma and Alzheimer's -
Claim 6; Page 280-281; 290pp; English.
ABL39691 to ABL39818 represent novel human nucleic acid sequences
encoding the proteins given in ABL06037 to ABL06164. The novel sequences
(NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,
anorectic, muscular, anti-HIV, antinfertility, cardiovascular,
anticoagulant, antibrinolytic, hypotension, antiasthmatic, cardiant,
immunomodulator, anticonvulsant, antidiabetic, tranquilliser, antiulcer,
antidepressant, gastrointestinal, neuroleptic, cerebroprotective,
nootropic and contraceptive activities. The NS can be used in vaccines,
gene therapy and antitense therapy. Nucleic acids, expression vectors and
antibodies from the present invention can be used for treating and
diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
disease, coagulation disease, ischaemia, hypertension, asthma, immune
disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
depression, schizophrenia, viral disease, gastric ulcers, stroke,
Alzheimer's disease and as a contraceptive.
Sequence 266 AA;
Query Match 7.7%; Score 56; DB 23; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.9e-49;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPKNSKVTOREHSSHTESVADLLALEPVDYKQSVNLVAGEAGGKQKAVEELD 56

Db 43 MPKNSKVTOREHSSHTESVADLLALEPVDYKQSVNLVAGEAGGKQKAVEELD 98
RESULT 4
AAO05876
ID AAO05876 standard; Protein; 122 AA.
AC AAO05876;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 19768.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
OS Homo sapiens.
XX
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US04927.
XX
XX 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
PI
XX WPI; 2001-514838/56.
DR N-PSDB; AAI85807.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
XX Claim 20; SEQ ID NO 19768; 1399pp + Sequence Listing; English.
PS
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 122 AA;
Query Match 7.2%; Score 52; DB 22; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.3e-45;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 354 VLGFKANIMNEKCVENAELGYLNTNVLSDRLIPPHVNFSLTTKDYMEM 405
XX
Db 20 VLGFKANIMNEKCVENAELGYLNTNVLSDRLIPPHVNFSLTTKDYMEM 71
RESULT 5
ABB11188
ID ABB11188 standard; peptide; 143 AA.
XX

AC ABB11188;
 XX 11-JAN-2002 (first entry)
 DE Human neurotransmitter transporter homologue, SEQ ID NO:1558.
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnery; antiulcer.
 XX Homo sapiens.
 OS WO200157188-A2.
 PN 09-AUG-2001.
 XX 05-FEB-2001; 2001WO-US03800.
 PF 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Drmanac RT;
 PI WPI: 2001-457740/49.
 DR N-PSDB; ABA08432.
 XX Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer -
 XX Claim 20; Page 154; 1963pp; English.
 PS Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.

CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention.
 XX Sequence 143 AA;
 SQ Query Match 6.1%; Score 44; DB 22; Length 143;
 Best Local Similarity 100.0%; Pred. No. 7.4e-37;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 505 FLVGLLFVQSGNYFVTMDDYSATPLTLIVILENTAVIY 548
 DB 71 FLVGLLFVQSGNYFVTMDDYSATPLTLIVILENTAVIY 114
 RESULT 6
 AAM24377
 ID AAM24377 standard; Protein; 127 AA.
 XX AC AAM24377;
 XX 12-OCT-2001 (first entry)
 XX DE Rat EST encoded protein SEQ ID NO: 1902.
 XX KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition.
 XX OS Rattus sp.
 XX WO200154477-A2.
 XX 02-AUG-2001.
 XX 25-JAN-2001; 2001WO-US02687.
 XX 25-JAN-2000; 2000US-0491404.
 PR 17-JUL-2000; 2000US-0617746.
 PR 03-AUG-2000; 2000US-0631451.
 PR 15-SEP-2000; 2000US-0663870.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;
 DR WPI: 2001-476164/51.
 DR N-PSDB; AAH99036.
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -
 PT Claim 20; Page 1225; 1275pp; English.
 PS The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity, and for nutritional purposes. The present sequence is a
 CC protein of the invention.
 XX Sequence 127 AA;
 SQ Query Match 5.1%; Score 37; DB 22; Length 127;

XX
 (continued on next page)

CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention.

XX Sequence 185 AA;

Query Match 3.0%; Score 22; DB 22; Length 185;
 Best Local Similarity 100.0%; Pred. No. 5.9e-14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 FVQRSGNYFVTMFDDYSATLPL 532
 |||||
 Db 30 FVQRSGNYFVTMFDDYSATLPL 51

RESULT 9
 ABB57432
 ID ABB57432 standard; Protein; 188 AA.

XX AC ABB57432;

XX DT 15-MAR-2002 (first entry)

XX DE Human secreted protein encoding polypeptide SEQ ID NO 78.

XX Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
 KW antiparkinsonian; antischlicking; antianaemic; antiarthritic; cancer;
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO200183510-A1.

XX PD 08-NOV-2001.

XX PF 26-APR-2001; 2001WO-US13318.

XX PR 02-MAY-2000; 2000US-201194P.

XX PR 16-JUN-2000; 2000US-212142P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Komatsoulis G, Ruben SM, Rosen CA;

XX DR WPI; 2002-121886/16.

XX An isolated nucleic acid molecule encoding a human secreted protein
 PT (SP) is useful in preventing, treating or ameliorating a disorder e.g.,
 PT Alzheimer's disease and cancers -

PS Disclosure; Page 473; 496pp; English.

XX The invention relates to novel genes (ABL01566-ABL01594) and proteins
 CC (ABB57394-ABB57456) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;

CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.

XX SQ Sequence 188 AA;

Query Match 3.0%; Score 22; DB 23; Length 188;
 Best Local Similarity 100.0%; Pred. No. 6e-14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 FVQRSGNYFVTMFDDYSATLPL 532
 |||||
 Db 142 FVQRSGNYFVTMFDDYSATLPL 163

RESULT 10

ABB57433

ID ABB57433 standard; Protein; 188 AA.

XX AC ABB57433;

XX DT 15-MAR-2002 (first entry)

XX DE Human secreted protein encoding polypeptide SEQ ID NO 79.

XX Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
 KW antiparkinsonian; antischlicking; antianaemic; antiarthritic; cancer;
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO200183510-A1.

XX PD 08-NOV-2001.

XX PF 26-APR-2001; 2001WO-US13318.

XX PR 02-MAY-2000; 2000US-201194P.

XX PR 16-JUN-2000; 2000US-212142P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Komatsoulis G, Ruben SM, Rosen CA;

XX DR WPI; 2002-121886/16.

XX An isolated nucleic acid molecule encoding a human secreted protein
 PT (SP) is useful in preventing, treating or ameliorating a disorder e.g.,
 PT Alzheimer's disease and cancers -

PS Disclosure; Page 473-474; 496pp; English.

XX The invention relates to novel genes (ABL01566-ABL01594) and proteins
 CC (ABB57394-ABB57456) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.

XX Sequence 188 AA;

Query Match 3.0%; Score 22; DB 23; Length 188;
 Best Local Similarity 100.0%; Pred. No. 6e-14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 FVQRSGNYFVTMFDYSATLPL 532
 DB 142 FVQRSGNYFVTMFDYSATLPL 163
 |||||

RESULT 11

AAO21214
 ID AAO21214 standard; Protein; 259 AA.

XX AC AAO21214;

XX DT 19-JUL-2002 (first entry)

XX DE Sodium-dependent neurotransmitter transporter protein.

XX KW Antiparkinsonian; nootropic; neuroprotective; tranquiliser; vulnerary;
 KW cerebroprotective; human sodium-dependent neurotransmitter transporter;
 KW hybridising; central; peripheral nervous system disease; brain injury;
 KW cerebrovascular disease; Parkinson's disease; corticobasal degeneration;
 KW motor neuron disease; dementia; multiple sclerosis; post-stroke;
 KW traumatic brain injury; stroke; post-traumatic brain injury;
 KW small-vessel cerebrovascular disease; Alzheimer's disease; gene therapy.

XX OS Homo sapiens.

XX PN WO200229048-A2.

XX PD 11-APR-2002.

XX PF 04-OCT-2001; 2001WO-EPI1440.

XX PR 05-OCT-2000; 2000US-237689P.

XX PA (FARB) BAYER AG.

XX PI Kohler RH;

XX DR WPI; 2002-426112/45.

XX DR N-PSDB; AAL37763.

XX PT New human sodium-dependent neurotransmitter transporter polypeptide,
 PT the regulation of which is useful for treating central or peripheral
 PT nervous system diseases e.g. brain injuries, Parkinson's disease, and
 PT dementia

XX PS Claim 1; Fig 2; 98pp; English.

XX CC The invention relates to a purified human sodium-dependent
 CC neurotransmitter transporter polypeptide comprising a sequence of 259
 CC amino acids, given in the specification. A nucleic acid encoding the
 CC protein is useful for detecting a polynucleotide encoding the protein in
 CC a biological sample by hybridising the protein-encoding polynucleotide to
 CC a nucleic acid material of a biological sample to form a hybridisation
 CC complex, and detecting the hybridisation complex. The protein of the
 CC invention and its encoding gene are useful for screening for agents which
 CC decrease the activity of sodium-dependent neurotransmitter transporter
 CC polypeptide by contacting the test compound with the protein or its gene
 CC and detecting binding of the test compound to the protein or its gene. A
 CC vector comprising the polynucleotide of the invention or a reagent that
 CC modulates the activity of the protein or its gene is useful for the
 CC preparation of a medicament for modulating the activity of sodium-
 CC dependent neurotransmitter transporter in a disease. The reagent is
 CC useful for treating diseases such as central or peripheral nervous system
 CC disease, where the central nervous system disorders are selected from
 CC brain injuries, cerebrovascular diseases and their consequences,
 CC Parkinson's disease, corticobasal degeneration, motor neuron disease,
 CC dementia, including multiple sclerosis, traumatic brain injury, stroke,
 CC post-stroke, post-traumatic brain injury, small-vessel cerebrovascular

CC disease, and Alzheimer's disease. The polynucleotide of the invention can
 CC be used in gene therapy. This sequence represents the 259 amino acid
 CC sodium-dependent neurotransmitter transporter protein of the invention.

XX SQ Sequence 259 AA;

Query Match 3.0%; Score 22; DB 23; Length 259;
 Best Local Similarity 100.0%; Pred. No. 8e-14;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 FVQRSGNYFVTMFDYSATLPL 532

DB 220 FVQRSGNYFVTMFDYSATLPL 241
 |||||

RESULT 12

AAG64743
 ID AAG64743 standard; Protein; 392 AA.

XX AC AAG64743;

XX DT 25-SEP-2001 (first entry)

XX DE Human sodium neurotransmitter cotransporter protein 8,43.

XX KW Human; sodium neurotransmitter cotransporter protein 8,43; cytostatic;
 KW virucidal; immunomodulatory; antiinflammatory; haemostatic;
 KW malignant tumour; haemopathy; HIV infection; immunological disease;
 KW inflammatory condition.

XX OS Homo sapiens.

XX PN WO200153496-A1.

XX PD 26-JUL-2001.

XX PF 15-JAN-2001; 2001WO-CN00020.

XX PR 21-JAN-2000; 2000CN-0111469.

XX PA (BIOD-) BIODOOR GENE TECHNOLOGY LTD SHANGHAI.

XX PI Mao Y, Xie Y;

XX DR WPI; 2001-465376/50.

XX DR N-PSDB; AAH73714.

XX PT Human sodium neurotransmitter cotransporter protein 8,43 and encoded
 PT polynucleotide, applicable in diagnosis and treatment of malignant
 PT tumor, hemopathy, HIV infection, immunological diseases and various
 PT inflammations

XX PS Claim 1; Page 33-34; 40pp; Chinese.

XX CC This invention relates to human sodium neurotransmitter cotransporter
 CC protein 8,43 and the cDNA encoding it. Included in the invention is a
 CC vector containing the cDNA, a host cell transformed with the vector and
 CC an antibody targeting the protein. The protein, polynucleotide, antibody,
 CC or ant/agonist can be used to achieve cytostatic; virucidal;
 CC immunomodulatory; antiinflammatory or haemostatic activity. They can be
 CC used in the diagnosis and treatment of malignant tumours, haemopathy, HIV
 CC infection, immunological diseases and various inflammatory conditions.
 CC The present sequence represents the human sodium neurotransmitter
 CC cotransporter protein 8,43.

XX SQ Sequence 392 AA;

Query Match 3.0%; Score 22; DB 22; Length 392;
 Best Local Similarity 100.0%; Pred. No. 1.2e-13;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 FVQRSGNYFVTMFDYSATLPL 532

|||||

Db 220 FVQRSGNYFTMTFDDYSATLPL 241

RESULT 13

AAO21215
ID AAO21215 standard; Protein: 729 AA.

XX AC AAO21215;

XX DT 19-JUL-2002 (first entry)

XX DE Protein sequence identified by SwissProt Accession No: Q08469.

XX KW Antiparkinsonian; nootropic; neuroprotective; tranquiliser; vulnary;
KW cerebroprotective; human sodium-dependent neurotransmitter transporter;
KW hybridising; central; peripheral nervous system disease; brain injury;
KW cerebrovascular disease; Parkinson's disease; corticobasal degeneration;
KW motor neuron disease; dementia; multiple sclerosis; post-stroke;
KW traumatic brain injury; stroke; post-traumatic brain injury;
KW small-vessel cerebrovascular disease; Alzheimer's disease; gene therapy.

XX OS Homo sapiens.

XX PN WO200229048-A2.

XX PD 11-APR-2002.

XX PF 04-OCT-2001; 2001WO-EP11440.

XX PR 05-OCT-2000; 2000US-237689P.

XX PA (FARB) BAYER AG.

XX PI Kohler RH;

XX WPI; 2002-426112/45.

XX PT New human sodium-dependent neurotransmitter transporter polypeptide,
PT the regulation of which is useful for treating central or peripheral
PT nervous system diseases e.g. brain injuries, Parkinson's disease, and
PT dementia

XX PS Disclosure; Fig 3; 98pp; English.

CC The invention relates to a purified human sodium-dependent
CC neurotransmitter transporter polypeptide comprising a sequence of 259
CC amino acids, given in the specification. A nucleic acid encoding the
CC protein is useful for detecting a polynucleotide encoding the protein in
CC a biological sample by hybridising the protein-encoding polynucleotide to
CC a nucleic acid material of a biological sample to form a hybridisation
CC complex, and detecting the hybridisation complex. The protein of the
CC invention and its encoding gene are useful for screening for agents which
CC decrease the activity of sodium-dependent neurotransmitter transporter
CC polypeptide by contacting the test compound with the protein or its gene
CC and detecting binding of the test compound to the protein or its gene. A
CC vector comprising the polynucleotide of the invention or a reagent that
CC modulates the activity of the protein or its gene is useful for the
CC preparation of a medicament for modulating the activity of sodium-
CC dependent neurotransmitter transporter in a disease. The reagent is
CC useful for treating diseases such as central or peripheral nervous system
CC disease, where the central nervous system disorders are selected from
CC brain injuries, cerebrovascular diseases and their consequences,
CC Parkinson's disease, corticobasal degeneration, motor neuron disease,
CC dementia, including multiple sclerosis, traumatic brain injury, stroke,
CC post-stroke, post-traumatic brain injury, small-vessel cerebrovascular
CC disease, and Alzheimer's disease. The polynucleotide of the invention can
CC be used in gene therapy. This sequence represents the protein sequence
CC identified by SwissProt Accession No: Q08469 relating to the sodium-
CC dependent neurotransmitter transporter protein of the invention.

XX SQ Sequence 729 AA;

Query Match 3.0%; Score 22; DB 23; Length 729;

Best Local Similarity 100.0%; Pred. No. 2.le-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 FVQRSGNYFTMTFDDYSATLPL 532

Db 512 FVQRSGNYFTMTFDDYSATLPL 533

RESULT 14

AAAG67159

ID AAG67159 standard; Protein: 730 AA.

XX AC AAG67159;

XX DT 13-NOV-2001 (first entry)

XX DE Amino acid sequence of a human 579 transporter polypeptide.

XX KW Human; transporter; 20685; 579; 17114; 23821; 33894; 32613;
KW vesicular monoamine transporter; neurotransmitter-symporter;
KW ABC transporter; sulfate transporter; Parkinson's disease; depression; pain;
KW central nervous system disorder; Parkinson's disease; neurological disorder;
KW infectious disease; cell proliferative disorder; spleen disorder; lung disorder;
KW immune disorder; inflammatory disorder; chronic bronchitis; ischemia;
KW Hodgkin's disease; Niemann-Pick disease; endometrium disorder;
KW colon disorder; cirrhosis; uterus disorder; brain disorder; T-cell disorder; anemia;
KW endometrial stromal tumour; skin disorder; lupus erythematosus; heart disorder;
KW Sjogren syndrome; haematopoietic stem cell; Alzheimer's disease; myocardial infarction;
KW blood vessel; Kawasaki syndrome; red cell disorder; thymus disorder;
KW B-cell disorder; kidney disorder; glomerulonephritis; breast disorder;
KW testis disorder; thyroid disorder; Graves disease; pancreatitis;
KW skeletal muscle disorder; tumour; pancreas disorder;
KW small intestine disorder; celiac sprue.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 61..659 /note= "sodium neurotransmitter-symporter domain"

FT Domain 70..87 /note= "transmembrane domain"

FT Domain 98..117 /note= "transmembrane domain"

FT Domain 140..164 /note= "transmembrane domain"

FT Domain 228..244 /note= "transmembrane domain"

FT Domain 253..275 /note= "transmembrane domain"

FT Domain 306..323 /note= "transmembrane domain"

FT Domain 334..358 /note= "transmembrane domain"

FT Domain 458..479 /note= "transmembrane domain"

FT Domain 496..513 /note= "transmembrane domain"

FT Domain 527..550 /note= "transmembrane domain"

FT Domain 575..594 /note= "transmembrane domain"

FT Domain 617..639 /note= "transmembrane domain"

XX WO200164875-A2.

XX PD 07-SEP-2001.

XX PF 28-FEB-2001; 2001WO-US06374.

XX PR 29-FEB-2000; 2000US-0185906.

PR 15-SEP-1999; 99GB-0021833.
 PR 17-MAR-2000; 2000GB-0006545.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX Hill J, Duckworth DM, Farmer M, Pangalos M;
 XX WPI: 2001-244780/25.
 DR N-PSDB; RAD03039.
 DR Novel NNT7 polypeptide useful for treating anxiety, depression,
 XX schizophrenia, phobia, parkinson's disease, stroke, pain, and
 PT psychiatric, panic, neurological, central nervous system, obsessive
 PT compulsive and sleep disorders
 XX Claim 3; Page 20; 27pp; English.
 PS The present sequence is human NNT7 protein encoded by a cDNA. NNT7 is
 XX thought to be a member of the neurotransmitter family of polypeptides.
 CC NNT7 sequences are useful for treating psychiatric disorders, anxiety,
 CC depression, schizophrenia, phobias, panic disorder, obsessive compulsive
 CC disorder, parkinson's disease, central nervous system disorders, stroke,
 CC neurological disorders, pain, neuropathic pain, sleep disorders, and
 CC diseases in which neurotransmitters are implicated. NNT7 sequences are
 CC useful for screening antagonists and agonists of NNT7 and as vaccines
 CC for inducing immunological response in a mammal. NNT7 sequences and its
 CC antibodies are useful to configure screening methods for detecting the
 CC effect of added compounds on the production of mRNA and polypeptide in
 CC cells. NNT7 is useful in conventional low capacity screening methods and
 CC also in high-throughput screening (HTS) formats and is useful for
 CC identifying membrane bound or soluble receptors. NNT7 antibody is useful
 CC to isolate or identify clones expressing NNT7 or to purify NNT7 by
 CC affinity chromatography. NNT7 is useful as diagnostic reagent for
 CC detecting mutations in the associated gene, and for chromosome
 CC localisation studies and tissue expression studies.
 XX Sequence 730 AA;
 SQ Query Match 3.0%; Score 22; DB 22; Length 730;
 Best Local Similarity 100.0%; Pred. No. 2.1e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 511 FVORSGNYFVTMFDDYSATLPL 532
 DB 512 FVORSGNYFVTMFDDYSATLPL 533
 Search completed: April 21, 2003, 14:09:56
 Job time : 43 secs

PA (MILL-) MILLENNIUM PHARM INC.
 XX Glucksmann MA;
 XX WPI: 2001-550178/61.
 DR N-PSDB; AAH/5186.
 DR Novel human transporter polypeptides useful for treating and diagnosing
 XX Parkinson's disease, Hodgkin disease, glomerulonephritis, myocardial
 PT infarction, Grave's disease, Alzheimer's disease, anemia, asthma and
 PT tumours
 XX Claim 9; Fig 9A-C; 259pp; English.
 PS The present sequence represents a human transporter polypeptide. The
 XX specification describes 20685, 579, 17114, 23821, 33894 or 32613 human
 CC transporter polypeptides. The 20685 transporter is similar to vesicular
 CC monoamine transporters. The 579 transporter is similar to
 CC neurotransmitter-symporters. The 17114 transporter is similar to ABC
 CC transporters. The 32613 transporter is similar to sulfate transporters.
 CC The transporter polypeptides and polynucleotides are useful for treating
 CC and diagnosing neurological and central nervous system disorders (e.g.
 CC Parkinson's disease, depression, pain), infectious diseases, cell
 CC proliferative disorders (e.g., cancer), blood disorders, and immune and
 CC inflammatory disorders. They are also useful for treating and
 CC diagnosing disorders involving the spleen (e.g., Hodgkin disease,
 CC Niemann-Pick disease), lung (e.g., chronic bronchitis), colon
 CC (cirrhosis), uterus and endometrium (e.g., endometrial stromal tumours),
 CC brain (e.g., ischemia), T-cells (e.g., Sjogren syndrome), skin (lupus
 CC erythematosus), haematopoietic stem cells (e.g., Alzheimer's disease),
 CC heart (e.g., myocardial infarction), blood vessels (e.g., Kawasaki
 CC syndrome), red cells (e.g., anemias), disorders involving thymus,
 CC B-cells, kidney (e.g., glomerulonephritis), disorders involving breast,
 CC testis, epididymis, prostate, thyroid (e.g., Graves disease), disorders
 CC involving skeletal muscle (e.g., tumour), pancreas (e.g., pancreatitis),
 CC small intestine (e.g., celiac sprue), disorders related to reduced
 CC platelet number and ovary.
 XX Sequence 730 AA;
 SQ Query Match 3.0%; Score 22; DB 22; Length 730;
 Best Local Similarity 100.0%; Pred. No. 2.1e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 511 FVORSGNYFVTMFDDYSATLPL 532
 DB 512 FVORSGNYFVTMFDDYSATLPL 533
 RESULT 15
 AAY72908
 ID AAY72908 standard; Protein; 730 AA.
 XX AC AAY72908;
 XX DT 13-JUN-2001 (first entry)
 XX DE Human NNT7 protein.
 XX Human; NNT7 protein; therapy; psychiatric disorder; anxiety; depression;
 KW schizophrenia; phobia; panic disorder; obsessive compulsive disorder;
 KW Parkinson's disease; central nervous system disorder; cerebroprotective;
 KW neurological disorder; stroke; pain; neuropathic pain; sleep disorder;
 KW tranquiliser; analgesic; neuroleptic; vaccine.
 XX OS Homo sapiens.
 XX PN WO200119854-A2.
 XX PD 22-MAR-2001.
 XX PF 14-SEP-2000; 2000WO-GB03541.
 XX

